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OM protein - protein search, using sw model

Run on: January 6, 2005, 13:24:17 ; Search time 154 Seconds
(without alignments)
333.106 Million cell updates/sec

Title: US-09-913-569B-6
Perfect score: 756
Sequence: 1 MVHGTIEVLVAGKLENTD.....PEDTRQGLPEDFGWKQSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1980s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	100.0	143	3 AAB44496	Aab44496 Plant vir
2	672	88.9	130	3 AAB44511	Aab44511 Plant vir
3	580.5	76.8	144	7 ADC53922	Adc53922 Rice phlo
4	575.5	76.1	144	3 AAB44498	Aab44498 Plant vir
5	523	69.2	129	3 AAB44495	Aab44495 Plant vir
6	523	69.2	145	6 AAE35936	Aae35936 Lolium pe
7	493	65.2	128	6 AAE35945	Aae35945 Lolium pe
8	483.5	64.0	147	3 AAG15489	Aag15489 Arabidops
9	470.5	62.2	202	3 AAB44510	Aab44510 Plant vir
10	459	60.7	130	3 AAB44494	Aab44494 Plant vir
11	454.5	60.1	145	3 AAB44507	Aab44507 Plant vir
12	445	58.9	140	3 AAB44497	Aab44497 Plant vir
13	429.5	56.8	142	3 AAB44509	Aab44509 Plant vir
14	419.5	55.5	133	3 AAG15297	Aag15297 Arabidops
15	404.5	53.5	149	3 AAB44508	Aab44508 Plant vir
16	398.5	52.7	123	3 AAG15490	Aag15490 Arabidops
17	368	48.7	187	3 AAB44512	Aab44512 Plant vir
18	328.5	43.5	102	3 AAG15298	Aag15298 Arabidops
19	325.5	43.1	102	3 AAG15491	Aag15491 Arabidops
20	278.5	36.8	157	3 AAB44501	Aab44501 Plant vir
21	271.5	35.9	151	3 AAB44504	Aab44504 Plant vir
22	260.5	34.5	154	3 AAB44505	Aab44505 Plant vir
23	260	34.4	154	3 AAB44503	Aab44503 Plant vir
24	249	32.9	156	7 ADC53926	Adc53926 Rice phlo
25	246	32.5	69	3 AAB44518	Aab44518 Plant vir

26	240.5	31.8	156	3 AAG54087	Aag54087 Arabidops
27	240.5	31.8	156	3 AAG11288	Aag11288 Arabidops
28	240.5	31.8	185	3 AAG54086	Aag54086 Arabidops
29	240.5	31.8	189	3 AAG11287	Aag11287 Arabidops
30	240.5	31.8	197	3 AAG23591	Aag23591 Arabidops
31	237.5	31.4	159	7 ADC53924	Adc53924 Rice phlo
32	220	29.1	102	3 AAB44502	Aab44502 Plant vir
33	205	27.1	89	3 AAB44515	Aab44515 Plant vir
34	175	23.1	85	3 AAB44514	Aab44514 Plant vir
35	166	22.0	244	3 AAG40015	Aag40015 Arabidops
36	166	22.0	245	3 AAG38059	Aag38059 Arabidops
37	166	22.0	245	3 AAG05889	Aag05889 Arabidops
38	166	22.0	247	3 AAG38058	Aag38058 Arabidops
39	166	22.0	247	3 AAG05888	Aag05888 Arabidops
40	166	22.0	263	3 AAG38057	Aag38057 Arabidops
41	166	22.0	274	3 AAG05887	Aag05887 Arabidops
42	156	20.6	99	3 AAB44516	Aab44516 Plant vir
43	150	19.8	258	3 AAB44500	Aab44500 Plant vir
44	127	16.8	308	3 AAB44499	Aab44499 Plant vir
45	125.5	16.6	466	4 AAB93562	Aab93562 Human pro

ALIGNMENTS

RESULT 1
AAB44496
ID AAB44496 standard; protein; 143 AA.
XX AC AAB44496;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 6.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Zea mays.
XX
PN WQ200060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
(DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
DR
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79350.
Novel viral movement polypeptides and polynucleotides useful in field of plant molecular biology, for producing transgenic plants, to prepare antibodies and in immunological screening of cDNA expression libraries.
Claim 10; Page 36-37; 62pp; English.
Polynucleotide sequences AAC79348-C79375 encode plant viral movement proteins AAB4494-B44520. Some plant viruses have been shown to be able to establish systemic infections via movement proteins that utilize existing plant pathways to traffic macromolecules to surrounding cells. Proteins such as those of the invention are similar to viral movement proteins that function in the transport of nucleic acids from cell to cell. The plant viral movement proteins are useful for obtaining a nucleic acid fragment encoding a viral movement protein. Polynucleotides encoding the plant viral movement proteins are useful for positive selection of a transformed cell. The proteins are useful in the field of plant molecular biology, and in the preparation of antibodies against the proteins. The proteins are also useful for isolating cDNAs and genes

CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 756; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.3e-79;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVVGAKGLENTDYLNCMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

Db 1 MVHGTLEVLVVGAKGLENTDYLNCMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

Db 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

QY 121 TFTPEDTRQRLPEDFGWKQSS 143

Db 121 TFTPEDTRQRLPEDFGWKQSS 143

RESULT 2

AAB44511
ID AAB44511 standard; protein; 130 AA.

AC AAB44511;

XX 06-FEB-2001 (first entry)

XX Plant viral movement protein SEQ ID 36.

XX Plant viral movement protein; transport; transgenic plant;

KW viral resistance; cosuppression.

XX Zea mays.

XX WO200060088-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009110.

XX 07-APR-1999; 99US-0128092P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Krebbers E, Weng Z, Cahoon RE;

XX WPI; 2000-638467/61.

XX N-PSDB; AAC79365.

XX Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.

XX Claim 23; Page 53-54; 62pp; English.

XX Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes

CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 130 AA;

Query Match 88.9%; Score 672; DB 3; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.2e-69;
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVVGAKGLENTDYLNCMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

Db 1 MVHGTLEVLVVGAKGLENTDYLNCMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

Db 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

QY 121 TFTPEDTRQR 130

Db 121 TFTPEDTRKR 130

RESULT 3

ADC53922
ID ADC53922 standard; protein; 144 AA.

AC ADC53922;

XX 18-DEC-2003 (first entry)

XX Rice phloem protein of the invention #1.

KW Rice; phloem protein; Ca2+/phospholipid-combining domain; promoter;
KW transgenic plant; phloem-specific; exotic protein; virus MP-like gene.

XX Oryza sativa.

Key	Location/Qualifiers
FT Misc-difference 21	/note= "Encoded by TAC"
FT Misc-difference 28	/note= "Encoded by TAC"
FT Misc-difference 94	/note= "Encoded by TAT"
FT Misc-difference 104	/note= "Encoded by TAT"
FT Misc-difference 112	/note= "Encoded by TAC"

XX JP2002315582-A.

XX 29-OCT-2002.

XX 24-APR-2001; 2001JP-00126682.

XX 24-APR-2001; 2001JP-00126682.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-407228/39.

XX N-PSDB; ADC53921.

XX A new protein in rice phloem and its gene, a DNA, a promotor, a
PT transgenic plant.

XX Claim 3; SEQ ID NO 2; 18pp; Japanese.

XX The invention discloses a rice phloem protein having Ca2+/phospholipid-
CC combining domain. Also claimed is a DNA encoding the novel rice phloem
CC protein, a promoter comprising a 1288 or 1572 base pair sequence, given

CC in the specification, a transgenic plant transformed to express phloem-
CC specifically the novel rice phloem protein, preparation of the novel rice
CC phloem protein by using the transgenic plant, a transgenic plant which
CC produces, phloem-specifically, an exotic protein. The method is used for
CC producing an exotic protein specifically in the phloem of a plant. The
CC gene represents a new virus MP-like gene from rice. The sequence
CC presented is a rice phloem protein of the invention.
XX
SQ

Sequence 144 AA;

Query Match 76.8%; Score 580.5; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 5.9e-59;
Matches 110; Conservative 18; Mismatches 15; Indels 1; Gaps 1;
Qy 1 MVHGTLEVLVGAAGLENTDYLNCMDPVAIKCRSQEOKSSIAATGKTTPEWNEFIPTV 60
Db 1 MVQGTLEVLVGAAGLENTDYLNCMDPVAIKCRSQEOKSSVAGSGSDPEWNETFVSV 60
Qy 61 SDRTTDLVIKMDSDTGADDFVGEATIPLEAVYTERSIPPTLYNVVYKGYCGEIKVGL 120
Db 61 THNATELIIKMDSDSGTDDDFVGEATISLEAIWTEGSIPTVWNVVKEEWRGEIKVGL 120
Qy 121 TFTPEDTRQGL-PEDFGWKQSS 143
Db 121 TFTPEDDRGLSEEDIGWKQSS 144

RESULT 4
AAB44498
ID AAB44498 standard; protein; 144 AA.
XX
AC AAB44498;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 10.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Triticum aestivum.
XX
PN WO2000060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Knebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79352.
XX
PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 38-39; 62pp; English.
XX

CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of

CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ

Sequence 144 AA;

Query Match 76.1%; Score 575.5; DB 3; Length 144;
Best Local Similarity 74.3%; Pred. No. 2.2e-50;
Matches 107; Conservative 17; Mismatches 19; Indels 1; Gaps 1;
Qy 1 MVHGTLEVLVGAAGLENTDYLNCMDPVAIKCRSQEOKSSIAATGKTTPEWNEFIPTV 60
Db 1 MAOGTLEVLVGAAGLENTDYLNCMDPVAIKCTSQEOKSTVAGSGSDPEWNETFVTV 60
Qy 61 SDRTTDLVIKMDSDTGADDFVGEATIPLEAVYTERSIPPTLYNVVYKGYCGEIKVGL 120
Db 61 SENATELVIKLDSDGGTDDSVGEATIPLDGVVTEGSIPTVWNVVYKGYCGEIKVGL 120
Qy 121 TFTPEDTRQGL-PED-FGHWKQSS 143
Db 121 TFTPEDARDQDQPEENYGGWQSS 144

RESULT 5
AAB44495
ID AAB44495 standard; protein; 129 AA.
XX
AC AAB44495;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 4.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Zea mays.
XX
PN WO2000060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Knebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79349.
XX
PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 35-36; 62pp; English.
XX

CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of

CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control coexpression and engineer plant virus resistance
XX
SQ Sequence 129 AA;

Query Match 69.2%; Score 523; DB 3; Length 129;
Best Local Similarity 78.6%; Pred. No. 2.4e-52;
Matches 99; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSIATGKTTPWNNFIPTV 60
DB 1 MAQGTLEVLVGAAGLENTDYLNNMDPYALQCRSHQKSSVAGSGCEPEWNETFTV 60

QY 61 SDRTDLVILKMSDGTGADDFVGEATIPLEAVVTERSIPPTLYNVVKGKYGCIKVL 120
DB 61 SDGAAELFIKLLSDGTDGDDFVGEATIPLEAVVTEGNIPTVYVNVKDEYRGEIKVL 120

QY 121 TFTPED 126
DB 121 TFTPED 126

RESULT 6
AAE35936
ID AAE35936 standard; protein; 145 AA.
XX
AC AAE35936;
XX
DT 17-JUN-2003 (first entry)
XX
DE Lolium perenne elicitor-responsive protein a (LpEra) protein.
XX
KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
KW protein storage; pest resistance; genetic marker; gene therapy; antipest;
KW agricultural; LpEra.
XX
OS Lolium perenne.
XX
PN WO200288359-A1.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-AU000539.
XX
PR 02-MAY-2001; 2001AU-00004735.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2003-201227/19.
DR N-PSDB; AAD54386.
XX

PT New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
PS Claim 18; Fig 17; 195pp; English.
XX
CC The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC

CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
CC protein
XX
SQ Sequence 145 AA;

Query Match 69.2%; Score 523; DB 6; Length 145;
Best Local Similarity 69.6%; Pred. No. 2.9e-52;
Matches 96; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 4 GTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSIATGKTTPWNNFIPTVSDR 63
DB 5 GTLEVLVGAAGLENTDYLNNMDPYALLVNTNEQRSSVAEGKSGEPENNETFVTTSN 64

QY 64 TTDLVILKMSDGTGADDFVGEATIPLEAVVTERSIPPTLYNVVKGKYGCIKVL 123
DB 65 ATELCIKLLDDDDGDDVGEARIPDLAVYTEGSIPTVYVNVKDEYCGEIRIGLKT 124

QY 124 PEDTRQGLPEDFGGWQ 141
DB 125 PEEAYHLLPEENFGWRQ 142

RESULT 7
AAE35945
ID AAE35945 standard; protein; 128 AA.
XX
AC AAE35945;
XX
DT 17-JUN-2003 (first entry)
XX
DE Lolium perenne elicitor-responsive protein a (LpEra).
XX
KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
KW protein storage; pest resistance; genetic marker; gene therapy; antipest;
KW agricultural; LpEra.
XX
OS Lolium perenne.
XX
PN WO200288359-A1.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-AU000539.
XX
PR 02-MAY-2001; 2001AU-00004735.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2003-201227/19.
DR N-PSDB; AAD54408.
XX

PT New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
PS Claim 18; Fig 50; 195pp; English.
XX
CC The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
CC protein
XX


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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148694P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 08-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 23-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161920P.

PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 64.0%; Score 483.5; DB 3; Length 147;
Best Local Similarity 65.0%; Pred. No. 1.2e-47;
Matches 93; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 1 MVHGTLEVLVVGAKGLENTDYLCNNDPPYAILKCRSQEQKSSATATGKGTTPWNNFIPTV 60
DB 1 MPHGTLEVLVLSAKGLEADADFLNNMDPPYVQLTCRTQDQKSNVAEGNGTTPWNETFIPTV 60
QY 61 SDRTTDLVIKLMDSDTGTTADDFVGEATIPLEAVYTERSIPTLYNVVKGKCYGKEIKVGL 120
DB 61 SEGTTELKAKIFDKVGTEDDAVGEATIPLEPVFVEGSIPTTAYNVVKKDEEYKGEIWWAL 120
QY 121 TTPEDTRORGLPED-FGGWKOS 142
DB 121 SFKPSGNRSRGMDEBSYGGWKNS 143

RESULT 9
AAB44510
ID AAB44510 standard; protein; 202 AA.
XX
AC AAB44510;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 34.
XX
KW Plant viral movement protein; transport; transgenic plant;
XX
OS Zea mays.
XX
PN WO200060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79364.
XX
PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 23; Page 52; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
```

```
XX SQ Sequence 202 AA;
Query Match 62.2%; Score 470.5; DB 3; Length 202;
Best Local Similarity 72.2%; Pred. No. 5.8e-46;
Matches 91; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQKSSIAATGKTTPWNNENFIFTV 60
Db 76 MAQGTLEVLVGAAGLENTDYLNNMDPYALLQCRSHEQKSSVASKGCEPEWNETFVTV 135

OY 61 SDRTDVLKLMDSGTGADDFVGEATIPLEA-VYTERSIDPTLYNNVKGKYGKGEIKVG 119
Db 136 SNGAKELFIKLDSDGGTDDDFVGEATIPLEASLHGKFAFLPTVYNNVKGDEYRGEIKVG 195

OY 120 LTFPTPE 125
Db 196 LTFPTPE 201

RESULT 10
AAB44494
ID AAB44494 standard; protein; 130 AA.
XX
AC AAB44494;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 2.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Vitis sp.
XX
FN WO2000060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79348.
XX
Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 34-35; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
```

```
XX SQ Sequence 130 AA;
Query Match 60.7%; Score 459; DB 3; Length 130;
Best Local Similarity 65.9%; Pred. No. 6.9e-45;
Matches 8; Conservative 23; Mismatches 16; Indels 6; Gaps 2;

OY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQKSSIAATGKTTPWNNENFIFTV 60
Db 1 MPQGTLEVLVSAKLENTDFLCNMDPVVLTCTQKSSVASGKSGDPEWNEHFVTI 60

OY 61 SDRTDVLKLMDSGTGADDFVGEATIPLEAVYTERSI-PPTLYNNVKGKYGKGEIKVG 119
Db 61 SEGISELTIIKMDSDSGGDFVGEATIPLEALFTEGSLFSTGTMLLKTKYCGEIKVG 120

OY 120 LTFPTPE 131
Db 121 LTFPTPE 127

RESULT 11
AAB44507
ID AAB44507 standard; protein; 145 AA.
XX
AC AAB44507;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 28.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Oryza sativa.
XX
FN WO2000060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79361.
XX
Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 49; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
```

```
XX SQ Sequence 145 AA;
Query Match 60.1%; Score 454.5; DB 3; Length 145;
Best Local Similarity 65.2%; Pred. No. 2.7e-44;
Matches 90; Conservative 16; Mismatches 31; Indels 1; Gaps 1;

QY 1 MVHGTLVLLVGAAGLENTDYLGNMPPYAILKCRSQEOKSSIAITGKTTPEWNEPIFTV 60
Db 1 MVHGKLEVLVCAKGLDITDFLNDMDPYVILTCRTQEQKSSVAKGAGSPFWNETVFTV 60

QY 61 SDRTDLVLIKMSDGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120
Db 61 SDDVPQLNVKIMSDAFSADDFVGEANIPLEPVFLEGLSPPAHRVVVKEEKYCGEIKVAL 120

QY 121 TFTP-EDTRQGLPEDFG 137
Db 121 TFTPAAETRRHHNENEG 138

RESULT 12
AAB44497
ID AAB44497 standard; protein; 140 AA.
XX AC AAB44497;
XX DT 06-FEB-2001 (first entry)
XX DE Plant viral movement protein SEQ ID 8.
XX KW Plant viral movement protein; transport; transgenic plant;
XX KW viral resistance; cosuppression.
XX OS Hevea brasiliensis.
XX PN WO200060088-A2.
XX PD 12-OCT-2000.
XX PF 06-APR-2000; 2000WO-US009110.
XX PR 07-APR-1999; 99US-0128092P.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Kriebbers E, Weng Z, Cahoon RE;
XX WP1; 2000-638467/61.
XX DR N-PSDB; AAC79351.
XX PT Novel viral movement polypeptides and polynucleotides useful in field of
XX PT plant molecular biology, for producing transgenic plants, to prepare
XX PT antibodies and in immunological screening of cDNA expression libraries.
XX PS Claim 10; Page 38; 62pp; English.
XX CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
XX CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
XX CC to establish systemic infections via movement proteins that utilise
XX CC existing plant pathways to traffic macromolecules to surrounding cells.
XX CC Proteins such as those of the invention are similar to viral movement
XX CC proteins that function in the transport of nucleic acids from cell to
XX CC cell. The plant viral movement proteins are useful for obtaining a
XX CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
XX CC encoding the plant viral movement proteins are useful for positive
XX CC selection of a transformed cell. The proteins are useful in the field of
XX CC plant molecular biology, and in the preparation of antibodies against the
XX CC proteins. The proteins are also useful for isolating cDNAs and genes
XX CC encoding homologous proteins from the same or other plant species, and to
XX CC create transgenic plants in which the protein is presented at higher or
XX CC lower levels than normal or in cell types or developmental stages in
XX CC which they are not normally found. The proteins and nucleotide sequences
XX CC may be used to control cosuppression and engineer plant virus resistance
```

```
XX SQ Sequence 140 AA;
Query Match 58.9%; Score 445; DB 3; Length 140;
Best Local Similarity 68.0%; Pred. No. 3.2e-43;
Matches 83; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 4 GTLEVLVCAKGLNTDYLGNMPPYAILKCRSQEOKSSIAITGKTTPEWNEPIFTVSDR 63
Db 4 GTVEVLVCAKGLNTDFLNGVDPYVVLACRTQEQKSSVAKGSEPEWNEKFEVSDG 63

QY 64 TTDLVLIKMSDGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGLTFT 123
Db 64 DTFLTLKIMSDVGAADDFVGEATIPLEPLFLEGNLPSTAYKVVKEQYKGEITVGLTFT 123

QY 124 PE 125
Db 124 PE 125

RESULT 13
AAB44509
ID AAB44509 standard; protein; 142 AA.
XX AC AAB44509;
XX DT 06-FEB-2001 (first entry)
XX DE Plant viral movement protein SEQ ID 32.
XX KW Plant viral movement protein; transport; transgenic plant;
XX KW viral resistance; cosuppression.
XX OS Triticum aestivum.
XX PN WO200060088-A2.
XX PD 12-OCT-2000.
XX PF 06-APR-2000; 2000WO-US009110.
XX PR 07-APR-1999; 99US-0128092P.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Kriebbers E, Weng Z, Cahoon RE;
XX WP1; 2000-638467/61.
XX DR N-PSDB; AAC79363.
XX PT Novel viral movement polypeptides and polynucleotides useful in field of
XX PT plant molecular biology, for producing transgenic plants, to prepare
XX PT antibodies and in immunological screening of cDNA expression libraries.
XX PS Claim 10; Page 51; 62pp; English.
XX CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
XX CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
XX CC to establish systemic infections via movement proteins that utilise
XX CC existing plant pathways to traffic macromolecules to surrounding cells.
XX CC Proteins such as those of the invention are similar to viral movement
XX CC proteins that function in the transport of nucleic acids from cell to
XX CC cell. The plant viral movement proteins are useful for obtaining a
XX CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
XX CC encoding the plant viral movement proteins are useful for positive
XX CC selection of a transformed cell. The proteins are useful in the field of
XX CC plant molecular biology, and in the preparation of antibodies against the
XX CC proteins. The proteins are also useful for isolating cDNAs and genes
XX CC encoding homologous proteins from the same or other plant species, and to
XX CC create transgenic plants in which the protein is presented at higher or
XX CC lower levels than normal or in cell types or developmental stages in
XX CC which they are not normally found. The proteins and nucleotide sequences
XX CC may be used to control cosuppression and engineer plant virus resistance
```

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XX SQ Sequence 142 AA;
Query Match 56.8%; Score 429.5; DB 3; Length 142;
Best Local Similarity 57.3%; Pred. No. 2, 1e-41;
Matches 82; Conservative 23; Mismatches 37; Indels 1; Gaps 1;

QY 1 MVHGTEVLLVCAKGLNTDYLCNMDPYAILKCRSQEQKSIATGKTTPWNNENFIFTY 60
DB 1 MVRGKLEVLVSAKGLDDSDFFNSMDPYVILTCSRHEQKSTVASGAGSEPEWNETFFAV 60
QY 61 SDRTTDLVILKMDSTGTADDPVGEATIPLEAVYTERTSLNNVYKGYCSEIKVGL 120
DB 61 SGDAPELVKIMDSALSGADLVGEACIPLEAVLQEGSLPPAVHRVWVDEYRGEIKIAL 120
QY 121 TFTPEDTRQGLPEDFGKWKSS 143
DB 121 TFTPAAENEENE-EESYGGWNQST 142

RESULT 14
AAG15297
ID AAG15297 standard; protein; 133 AA.
XX AC AAG15297;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 15497.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
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PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 06-JUL-1999; 99US-0142390P.
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PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143342P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
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PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
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PR 21-JUL-1999; 99US-0144814P.
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PR 22-JUL-1999; 99US-0145085P.
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PR 23-JUL-1999; 99US-0145192P.
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PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 149 AA;

Query Match 53.5%; Score 404.5; DB 3; Length 149;
Best Local Similarity 52.1%; Pred. No. 1.8e-38;
Matches 76; Conservative 29; Mismatches 38; Indels 3; Gaps 1;
Qy 1 MVHGTLEVLLVGAKGLENLDYLCNMDPYAILKCRSQEQKSSIAATGKTTPEWNNENFIFTV 60
Db 1 MPRGTLEVLLISAKGIDNDLSSIDPVIITYRAQEKSTVQEDAGSKPQWNEFIFTV 60
Qy 61 SDRTDLVILKMDSDTGTADDFVGEATIPLEAVYTERSIPETLYNVVKGEYKCVGL 120
Db 61 SDSASELNLIKMDKDNFSQDDCLGEATIHLDVPFAGSIPETAYKVKVDEEYCGEIKVAL 120
Qy 121 TFTPEDTFRGL---PEDFGGWKQSS 143
Db 121 TFTAERNEEQYDAPEESYGGWKSS 146

Search completed: January 6, 2005, 13:59:22
Job time : 156 secs

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <STO>
C;Genetics:
A;Cross-references: UNIPROT:Q9C8S6; GB:AE005173; NID:96997198; PIDN:AAF34860.1; GSPDB:GN
A;Gene: F9N12.16
A;Map position: 1

Query Match 64.4%; Score 486.5; DB 2; Length 147;
Best Local Similarity 65.0%; Pred. No. 1.1e-39;
Matches 93; Conservative 17; Mismatches 32; Indels 1; Gaps 1;

QY 1 MVHGTEVLVVGAKGLENTDYLGNMPPYAILKCRSQEQKSSATGKTTPWNNENFIPTV 60
Db 1 MPHGTEVLVLSAKGLEADFLNMDPYVOLTCTQDKSNVAGMGTTPEWNETIFTV 60

QY 61 SDRTTDLVVKLMSDGTADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKYGKIKVGL 120
Db 61 SEGTTLLKAKIFDKDVGTEDDAVGEATIPLEPVFVSGSIPPTAYNVVKKDEYKGEIIVAL 120

QY 121 TFTPEDTRQGLPED-FCGWKQS 142
Db 121 SFKPSNRSRGMDSESYGGWKNS 143

RESULT 3
T04091
hypothetical protein - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04091
R;Betawar, N.M.; Baysdorfer, C.
submitted to the EMBL Data Library, July 1996
A;Description: Novel maize gene.
A;Reference number: Z15202
A;Accession: T04091
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-143 <BET>
A;Cross-references: UNIPROT:Q24582; EMBL:U64437; NID:gl498054; PIDN:AAB06331.1; PID:g149
A;Experimental source: strain B73

Query Match 60.3%; Score 455.5; DB 2; Length 143;
Best Local Similarity 62.1%; Pred. No. 1e-36;
Matches 90; Conservative 18; Mismatches 28; Indels 9; Gaps 3;

QY 1 MVHGTEVLVVGAKGLENTDYLGNMPPYAILKCRSQEQKSSATGKTTPWNNENFIPTV 60
Db 1 MVHGTEVLVLSAKGLEDTDFLNMDPPVILTCTQEQKSSVANGAGSEPNWNETFVFTV 60

QY 61 SDRTTDLVVKLMSDGTADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKYGKIKVGL 120
Db 61 SDTTPQLHUKIMSDL-TNDDFVGERTIPLEAVFOGSLPPAVHPVVKEEKYCGEYKLLAL 119

QY 121 TFTPEDTRQGLPED-----FCGW 139
Db 120 TFTPAAETRR--PDDNEEGPPYSSW 142

RESULT 4
T04363
FIERG2 protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04363
R;Kim, C.Y.; Choe, M.S.; Jeong, S.Y.; Bae, C.G.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
submitted to the EMBL Data Library, March 1997
A;Description: Isolation and characterization of early rice genes by a fungal elicitor
A;Reference number: Z15277
A;Accession: T04363
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-156 <KIM>
A;Cross-references: UNIPROT:O50006; EMBL:U95136; NID:g2920838; PIDN:AAC04628.1; PID:g29.
C;Genetics:
A;Gene: FIERG2

Query Match 34.3%; Score 259; DB 2; Length 156;
Best Local Similarity 41.3%; Pred. No. 1e-17;
Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;

QY 4 GTLEVLVVGAKGLENTDYLGNMPPYAILKCRSQEQKSSATGKTTPWNNENFIPTVSDR 63
Db 5 GVLEVHLVDKAGLGTGNDFLGKIDPVVQYRSQERKSSVARQDQKNPSWNEVFKFQINST 64

QY 64 TT-----DLVVKLMSDGTADDFVGEAT-----IPLEAVYTTERSIPPTLYNVVKGK-Y 112
Db 65 AATGQHLFLRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWMSSESKHRVVLADKTY 124

QY 113 CGEIKVGLTFTPTEDTRQGLPEDFCGWKQS 142
Db 125 HGEIRVSLTFT-ASAKADHAEQVGVGWAHS 153

RESULT 5
T04314
FIERG1 protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04314
R;Kim, C.Y.; Choe, M.S.; Jeong, S.Y.; Bae, C.G.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
submitted to the EMBL Data Library, March 1997
A;Description: Isolation and characterization of early rice genes by a fungal elicitor
A;Reference number: Z15277
A;Accession: T04314
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-159 <KIM>
A;Cross-references: UNIPROT:O50005; EMBL:U95135; NID:g2920836; PIDN:AAC04627.1; PID:g29.
C;Genetics:
A;Gene: FIERG1
A;Note: fungal inducible gene

Query Match 32.6%; Score 246.5; DB 2; Length 159;
Best Local Similarity 40.5%; Pred. No. 1.6e-16;
Matches 62; Conservative 22; Mismatches 54; Indels 15; Gaps 5;

QY 4 GTLEVLVVGAKGLENTDYL---CNMDPYAILKCRSQEQKSSATGKTTPWNNENFIPTV 60
Db 5 GVLEVHLVDKAGLGTGNDFLGKIDPVVQYRSQERKSSVARQDQKNPSWNEVFKFQI 64

QY 61 SDRIT- ---DLVVKLMSDGTADDFVGEAT-----IPLEAVYTTERSIPPTLYNVVKGK 110
Db 65 NSTAATGQHKLFRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWMSSESKHRVVLAD 124

QY 111 K-YCGEIKVGLTFTPTEDTRQGLPEDFCGWKQS 142
Db 125 KTYHGEIRVSLTFT-ASAKADHAEQVGVGWAHS 156

RESULT 6
T047686
elicitor responsive/phloem-like protein - Arabidopsis thaliana
N;Alternate names: protein T22E16.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T047686
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lencke, K.; Mayer, K.I.
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24472
A;Accession: T047686
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <BEN>
A;Cross-references: UNIPROT:Q9M2T2; EMBL:AL132975

A;Experimental source: cultivar Columbia; BAC clone T22E16
C;Genetics:
A;Map position: 3
A;Introns: 23/1; 45/1; 92/2; 137/3
A;Note: T22E16.130

Query Match 31.8%; Score 240.5; DB 2; Length 156;
Best Local Similarity 35.5%; Pred. No. 6.1e-16;
Matches 55; Conservative 33; Mismatches 52; Indels 15; Gaps 6;

Qy 1 MVHCTLEVLVGAGLENTDYLNCMDPYAILKCRSQEQKSSIA-TGKGTTPWNNF--- 56

Db 1 MAVGILEVLSLGGKLRKSLDPLGIDPYVEIQYQGRKSKVAKEDGGRNPTWMDKLWR 60

Qy 57 -IFTVSDRTDVLKLMDSDTGTDADDFVGEATIPLEAVYT-----ERSIPPTLYNVVKG 109

Db 61 AEPFGSGADYKLVKVMHDHFTSSDDFGEATVHVKELLENGVEKGTAEALRPTKYNIIVDS 120

Qy 110 E-KYCGEIKVGLTTPEDTRQGLP-EDFGWKOS 142

Db 121 DLSFVGELLIGVSYSL--LQDRGMGDRQFGWKHS 153

RESULT 7

T50648

phloem protein [imported] - winter squash

C;Species: Cucurbita maxima (winter squash)

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C;Accession: T50648

R;Xoonostle-Cazares, B.; Xiang, Y.; Ruiz-Medrano, R.; Wang, H.L.; Monzer, J.; Yoo, B.C.

Science 283, 94-98, 1999

A;Title: Plant paralog to viral movement protein that potentiates transport of mRNA into

A;Reference number: 225155; MUID:99102700; PMID:9872750

A;Accession: T50648

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-150 <XOC>

A;Cross-references: UNIPROT:Q92T47; EMBL:AF079170; PIDN:AAD05496.1

A;Experimental source: cultivar Big max

C;Genetics:

A;Gene: PP16

Query Match 23.4%; Score 177; DB 2; Length 150;

Best Local Similarity 32.8%; Pred. No. 7.7e-10;

Matches 43; Conservative 27; Mismatches 49; Indels 12; Gaps 4;

Qy 4 GTLEVLVGAGLENTDYLCH-MDPYAILKCRSQEQKSSIATGKGTTPWNNFIFTV-- 60

Db 4 GMMEVHLISGKGLQAHPLNKPIDPYAEINFKGQGRMSKVAKNAGPNPLWDEKPKFLAEY 63

Qy 61 --SDRTTDLVKLMDSDTGTDADDFVGEATIPLEAVYTE-----RSIPPTLYNVVKG-K 111

Db 64 PGSGGDPHILFKVMHDHDAIGDDYIGVDKIDVKLLAEGVRKKGSEMPRMHYHLAKIH 123

Qy 112 YCGEIKVGLTF 122

Db 124 FKGEIEGVSP 134

RESULT 8

E86165

P15K9.2 protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E86165

R;Theologie, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86165

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1020 <STO>

A;Cross-references: UNIPROT:Q9ZVT9; GB:AB005172; NID:93850580; PIDN:AAC72128.1; GSPDB:G

C;Genetics:

A;Map position: 1

Query Match 19.8%; Score 149.5; DB 2; Length 1020;
Best Local Similarity 30.5%; Pred. No. 3.8e-06;
Matches 39; Conservative 27; Mismatches 55; Indels 7; Gaps 4;

Qy 6 LEVLLVGAKGLENTDYLNCMDPYAILKCRSQEQKSSIATGKGTTPWNNFIFTVSDRTT 65

Db 3 LQVRVVEARNLPAMDNLGFSDFVRLQLGKQRSTKVVK-KNLNPKWTEDEFSFGVDDLND 61

Qy 66 DLVILKLMDSDTGTDADDFVGEATIPLEAVY--TERSIPPTLYNV---VKG-EKYCGEIKVG 119

Db 62 ELVVSVLDEKYNDDFVGQVRVSVSLVFDENQSLGTVWYPLNPKKSKKDCGCEILLK 121

Qy 120 LTFPTPDT 127

Db 122 ICFSQKNS 129

RESULT 9

T05421

hypothetical protein F28A23.90 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05421

R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.;

submitted to the Protein Sequence Database, October 1998

A;Reference number: Z15415

A;Accession: T05421

A;Molecule type: DNA

A;Residues: 1-279 <BEV>

A;Cross-references: UNIPROT:O49490; EMBL:AL021961

A;Experimental source: cultivar Columbia; BAC clone F28A23

C;Genetics:

A;Map position: 4

A;Introns: 38/1; 73/1; 115/2; 139/2; 151/3

A;Note: F28A23.90

Query Match 19.2%; Score 145; DB 2; Length 279;
Best Local Similarity 32.6%; Pred. No. 2e-06;
Matches 28; Conservative 22; Mismatches 36; Indels 0; Gaps 0;

Qy 11 VGAGLENTDYLNCMDPYAILKCRSQEQKSSIATGKGTTPWNNFIFTVSDRTTDLVIK 70

Db 39 VGCCKLKTSEFRSQDPYVVLVEYGGRSRTRTCTDGGKNAVFOEKFIITLIEGLRDLKVA 98

Qy 71 LMSDSTGTADDVFGEATIPLEAVYTE 96

Db 99 VVNSNTLSTDDFIGNATIQLQKVLQ 124

RESULT 10

T51799

CLB1-like protein - Arabidopsis thaliana

N;Alternate names: protein T5K6_90

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: T51799

R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Voelckert, G.;

submitted to the Protein Sequence Database, August 2000

A;Reference number: Z25455

A;Accession: T51799

A;Status: preliminary

A;Molecule type: DNA


```
Db 158 AERSRVISDGLVQDVILRLRHVEGCEVEAQLQWI--DLPGKGL 200
RESULT 14
T25673
hypothetical protein D2092.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25673
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25673
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-804 <GAT>
A:Cross-references: UNIPROT:P91199; EMBL:U88167; PIDN:AAB42222.1; GSPDB:GN00019; CESP:D2092
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.1
A:Map position: 1
A:Introns: 34/3; 76/1; 150/2; 206/1; 218/1; 301/2; 451/1; 498/2; 589/3; 631/3; 686/3; 79
Query Match 15.7%; Score 118.5; DB 2; Length 804;
Best Local Similarity 26.4%; Pred. No. 0.0027;
Matches 38; Conservative 28; Mismatches 57; Indels 21; Gaps 6;
Qy 9 LLVCAKGLNTDYLCNMDPFAILK-CRSQEQKSSIAATGKTTPEWNNENFIYVSDRTDIL 67
Db 450 LVFGAEDLVAKDFGKSDPFAVLVNRVTQTNTIY--KTLSPSNKXIYTFAVKDIHTCL 507
Qy 68 VIKLMSDGTGADDFVGEATIPLEAVYTERSIPTLYNV-----VKGEKYC----- 113
Db 508 QVTIYDEDPNRRFELGRVQIPLKSI---RNCQKRWGLKDEKLKRVKGVLEMDVIV 564
Qy 114 GEIKVGL-TFTPEDTRQGLPEDF 136
Db 565 NPRAAIRTFKPKIKYMSQEQKF 588
RESULT 15
S70642
ubiquitin ligase Nedda - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S70642
R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.
EMBO J. 15, 2371-2380, 1996
A:Title: WW domains of Nedda bind to the proline-rich PY motifs in the epithelial Na(+)
A:Reference number: S70642; MUID:96221297; PMID:8665844
A:Accession: S70642
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-887 <STA>
A:Cross-references: UNIPROT:Q62940; EMBL:U50842; NID:gl293646; PIDN:AAB48949.1; PID:gl293646
C:Genetics:
A:Gene: Nedda4
C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin
F:54-167/Domain: protein kinase C C2 region homology <KC2>
F:246-283/Domain: WW repeat homology <WW1>
F:402-439/Domain: WW repeat homology <WW2>
F:459-496/Domain: WW repeat homology <WW3>
F:555-881/Domain: ubiquitin-protein ligase homology <UBI>
Query Match 15.5%; Score 117.5; DB 2; Length 887;
Best Local Similarity 24.3%; Pred. No. 0.0039;
Matches 33; Conservative 28; Mismatches 58; Indels 17; Gaps 4;
Qy 6 LEVLLVCAKGLNTDYLCNMDPFAILKCRSQEQKSSIAATG-----KGTTPWNNENFI 58
Db 77 VRVKVIAGIGLAKDILGASDPY--VRVTLYDPMSGLVTSVQTKTIKSLNPKWNEILF 134
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 13:49:13 ; Search time 41 Seconds
(without alignments)
231.304 Million cell updates/sec

Title: US-09-913-569B-6
Perfect score: 756
Sequence: 1 MVHGTLEVLVGAKGLENTD.....PEDTRQRLPEDFGMKQSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.5	16.2	927	3	US-08-895-601-6
2	113	14.9	1026	4	US-09-248-796A-16128
3	112.5	14.9	291	4	US-09-248-796A-15333
4	106	14.0	988	4	US-09-382-552-233
5	106	14.0	2080	4	US-09-382-552-2
6	104.5	13.8	82	4	US-09-382-552-88
7	104.5	13.8	799	3	US-08-909-954-4
8	102.5	13.6	672	4	US-10-092-138A-27
9	102.5	13.6	672	4	US-09-538-092-943
10	99.5	13.2	233	4	US-09-248-796A-18185
11	97.5	12.9	916	4	US-09-417-157-73
12	96.5	12.8	172	4	US-09-270-767-43037
13	96.5	12.8	766	3	US-08-539-205A-4
14	96.5	12.8	766	4	US-09-392-163A-4
15	96	12.7	673	4	US-09-538-092-853
16	95	12.6	623	4	US-09-270-767-45228
17	94.5	12.5	324	4	US-09-270-767-44986
18	92	12.2	744	3	US-09-738-884-5
19	92	12.2	744	4	US-10-096-961A-5
20	89.5	11.8	916	4	US-09-688-078-9
21	88.5	11.7	804	3	US-08-909-954-2
22	86.5	11.4	372	4	US-09-107-532A-6792
23	86.5	11.4	1154	4	US-09-688-078-7
24	86	11.4	349	4	US-09-270-767-45401
25	85	11.2	132	4	US-09-294-298A-17
26	85	11.2	744	3	US-09-738-884-4
27	85	11.2	744	4	US-10-096-961A-4

28	84.5	11.2	1001	4	US-09-688-078-2	Sequence 2, Appli
29	84	11.1	140	2	US-08-609-049A-16	Sequence 16, Appl
30	84	11.1	140	3	US-09-170-996-16	Sequence 16, Appl
31	84	11.1	641	3	US-09-422-869-26	Sequence 26, Appl
32	83.5	11.0	639	3	US-09-422-869-25	Sequence 25, Appl
33	83.5	11.0	640	4	US-09-308-345A-7	Sequence 7, Appli
34	83	11.0	336	4	US-09-270-767-33924	Sequence 33924, A
35	83	11.0	336	4	US-09-270-767-49141	Sequence 49141, A
36	83	11.0	671	6	5266464-2	Patent No. 5266464
37	81.5	10.8	640	4	US-09-308-345A-2	Sequence 2, Appli
38	77	10.2	1590	4	US-09-617-099B-1	Sequence 1, Appli
39	76.5	10.1	183	4	US-09-583-110-4832	Sequence 4832, Ap
40	76.5	10.1	205	4	US-09-270-767-42337	Sequence 42337, A
41	75.5	10.0	115	3	US-09-036-315-8	Sequence 8, Appli
42	75.5	10.0	422	3	US-08-872-979-8	Sequence 8, Appli
43	75	9.9	117	3	US-09-036-315-6	Sequence 6, Appli
44	75	9.9	812	1	US-08-446-794A-2	Sequence 2, Appli
45	75	9.9	812	1	US-08-750-007-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-895-601-6
; Sequence 6, Application US/08895601
; Patent No. 6060262
; GENERAL INFORMATION:
; APPLICANT: Beer-Romero, Peggy
; APPLICANT: Strack, Peter J.
; APPLICANT: Glass, Susan J.
; APPLICANT: Rolfe, Mark
; TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,
; TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,601
; FILING DATE: 16-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-096.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-895-601-6

Query Match 16.2%; Score 122.5; DB 3; Length 927;
Best Local Similarity 25.1%; Pred. No. 7.1e-06;
Matches 42; Conservative 25; Mismatches 69; Indels 31; Gaps 6;
Qy 2 VHGTLE-----VLLVGAKGLENTDYLCNMDPYAILKCRSQEQKSIATG----- 45
Db 35 VFGLEDENSRIVRVRIAGIGLAKDKILGASDPY--VRVTLYDPMNGVLTSTVQTKIK 92

; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2080
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-552-2

Query Match 14.0%; Score 106; DB 4; Length 2080;
Best Local Similarity 27.9%; Pred. No. 0.0025;
Matches 34; Conservative 20; Mismatches 52; Indels 16; Gaps 4;
Qy 6 LEVLLVGAKGLENLDYLCNMDPYAILKCRSQEQKSSATGKGT-TPWNNENFIF-----58
Db 1154 LRCYMYQARDLAAMDKDSFDPYAIVSPLHQSQKTVVV--KNTLNPTWDQTLIFYEIEIF 1211
Qy 59 ----TVSDRTTDLVILKMDSTGTADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYG 114
Db 1212 GEPATVAEQPPSIVVELYDHDYGADEFMGRICQPS---LERMPRLAWPEPLTRGSQPSG 1268
Qy 115 EI 116
Db 1269 EL 1270

RESULT 6
US-09-382-552-88
; Sequence 88, Application US/09382552
; Patent No. 6673909
; GENERAL INFORMATION:
; APPLICANT: Brown, Jr., Robert H.
; APPLICANT: Liu, Jing
; APPLICANT: Aoki, Masashi
; APPLICANT: Ho, Meng
; APPLICANT: Matsuda-Asada, Chie
; TITLE OF INVENTION: DYSFERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
; TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
; FILE REFERENCE: 00786/399002
; CURRENT APPLICATION NUMBER: US/09/382,552
; EARLIER FILING DATE: 1993-08-25
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-552-88

Query Match 13.8%; Score 104.5; DB 4; Length 82;
Best Local Similarity 35.7%; Pred. No. 3.4e-05;
Matches 25; Conservative 13; Mismatches 19; Indels 13; Gaps 3;
Qy 26 DPYAILKCRSQEQKSSATGKGT-TPWNNENFIF-----TVSDRTTDLVILKMDS 74
Db 15 DPYAIVSPLHQSQKTVVV--KNTLNPTWDQTLIFYEIEIFGEPATVAEQPPSIVVELYD 72
Qy 75 DTGTADDFVG 84
Db 73 DTGADDFVG 82

RESULT 7
US-08-909-954-4
; Sequence 4, Application US/08909954A
; Patent No. 6100058
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: GAP12 Genes and their Uses
; FILE REFERENCE: SEQ-11p

; CURRENT APPLICATION NUMBER: US/08/909,954A
; CURRENT FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 799
; TYPE: PRT
; ORGANISM: M. musculus
US-08-909-954-4

Query Match 13.8%; Score 104.5; DB 3; Length 799;
Best Local Similarity 23.4%; Pred. No. 0.00096;
Matches 36; Conservative 26; Mismatches 67; Indels 25; Gaps 4;
Qy 4 GTLEVLIVGAKGLENLDYLCNMDPYAILKCRSQEQKSSATGKGTTPWNNENFIFTVSDR 63
Db 5 GSLSIRVVEGRALPAKDVSGSDPYCLVKVDDQVVARTATWRSLSFPMGEEYTVHLPLD 64
Qy 64 TTDLVILKMDSDGTADDFVGEATIPLEAVYTTERSIPPTLYNV-----VKGEKYCGE 115
Db 65 FHLAFVYVLDVTGHHDIIGKISLSKEAITADPRGIDSWINLSRVDPAEVQGE-VCLD 123
Qy 116 IKVGLTFTPEDTRQGL-----PEDFGG 138
Db 124 VKL-----LEDARGRLCHVROARDLAPRDISG 152

RESULT 8
US-10-092-138A-27
; Sequence 27, Application US/10092138A
; Patent No. 6743630
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 65823/JPW/PT
; CURRENT APPLICATION NUMBER: US/10/092,138A
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 672
; TYPE: PRT
; ORGANISM: human
US-10-092-138A-27

Query Match 13.6%; Score 102.5; DB 4; Length 672;
Best Local Similarity 30.6%; Pred. No. 0.0013;
Matches 37; Conservative 14; Mismatches 49; Indels 21; Gaps 5;
Qy 6 LEVLLVGAKGLENLDYLCNMDPYAILKCR-----RSQEQKSSATGKGT-TPWNNENFIFTV- 60
Db 173 LHVTVRDARKNLIPMDPNGLSDPYVKULIPDPKNESKQKTKTIRSTLNPNWNESTFTPLK 232
Qy 61 -SDRTTDLVILKMDSDGTADDFVGEAT-----IPLEAVYTTERSIPPTLYNVVKGK 111
Db 233 PSDKDRRLSVEIWDWDRTRTTFNDPMGSLSCFVSELKMKMPASGWY-----KLLNQEGEY 285
Qy 112 Y 112
Db 286 Y 286

RESULT 9
US-09-538-092-943
; Sequence 943, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092

; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapSeqFormat Version 0.9
; SEQ ID NO 943
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P17252
US-09-538-092-943

Query Match 13.6%; Score 102.5; DB 4; Length 672;
Best Local Similarity 30.6%; Pred. No. 0.0013;
Matches 37; Conservative 14; Mismatches 49; Indels 21; Gaps 5;

QY 6 LEVLLVGAKGLENLDYLCNMDPYAILKC-----RSQEQKSSIAATGKGT-TPEWNNENFIFTV- 60
Db 173 LHVTVRDAKNLIPMDPNGLSDPYVKLIPDPKNESKQKTKTIRSTLNQWNESFTFKLK 232
QY 61 -SDRTTDLVIKLDSDTGTADDFVGEAT-----IPLAVYTTERSIPPTLYNNVKGK 111
Db 233 PSKDRRLSVEIWDWDRTRTRNDFMGLSFGVSELKMKMPASGWY-----KLLNQBEGEY 285

QY 112 Y 112
Db 286 Y 286

RESULT 10
US-09-248-796A-18185
; Sequence 18185, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18185
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18185

Query Match 13.2%; Score 99.5; DB 4; Length 233;
Best Local Similarity 33.3%; Pred. No. 0.00065;
Matches 23; Conservative 12; Mismatches 33; Indels 1; Gaps 1;

QY 5 TLEVLLVGAKGLENLDYLCNMDPYAILKCRSQEQKSSIAATGKGTTPWNNENFIFTVSDRT 64
Db 17 TINVKVAAESLYKRDVFRQDPDFAVLTVDGSGTKTTITAKTLNPNWNETNFQAKDS 76

QY 65 TDLVIKMD 73
Db 77 I-LVIQVDF 84

RESULT 11
US-09-417-197-73
; Sequence 73, Application US/09417197
; Patent No. 6518021

; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct
US-09-417-197-73

Query Match 12.9%; Score 97.5; DB 4; Length 916;
Best Local Similarity 26.4%; Pred. No. 0.0086;
Matches 32; Conservative 20; Mismatches 48; Indels 21; Gaps 4;

QY 6 LEVLLVGAKGLENLDYLCNMDPYAILKC-----RSQEQKSSIAATGKGTTPWNNENFIFTV- 60
Db 173 LHVTVRDAKNLIPMDPNGLSDPYVKLIPDPKNESKQKTKTIRSTLNQWNESFTFKLK 232
QY 61 -SDRTTDLVIKLDSDTGTADDFVGEAT-----IPLAVYTTERSIPPTLYNNVKGK 111
Db 233 PSKDRRLSVEIWDWDRTRTRNDFMGLSFGVSELKMKMPASGWY-----KAHNOBEGEY 285

QY 112 Y 112
Db 286 Y 286

RESULT 12
US-09-270-767-43037
; Sequence 43037, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43037
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43037

Query Match 12.8%; Score 96.5; DB 4; Length 172;
Best Local Similarity 28.0%; Pred. No. 0.00098;
Matches 40; Conservative 18; Mismatches 66; Indels 19; Gaps 6;

QY 16 LENTDYLCNMDPYAILKCRSQEQKSSI-----ATGKGT-TPEWNNENFIFTVSDRTDLVI 69
Db 2 LAKKDIFGASDPYVRAIDLNTINGDINIDSVLTTKKTKTLNPTWNEEFIFRVKPSHKLVF 61
QY 70 KLMSDTCGTADDFVGEATIPLEAVYTE---RSIPPTLY-----NVVKGKCYGGEIKVGL 120
Db 62 QVFENRLTRDDFLGNVELTLVNLPTQEGRTIGEQSTLPRRSVGAKSRIKGLTRIYH 121

QY 121 TFTPEDTRQGLP---EDFGGWK 140
Db 122 AFIRE-TREQSEPPSSGNSDGEWE 143

RESULT 13
US-08-539-205A-4
; Sequence 4, Application US/08539205A
; Patent No. 6001619

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;
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Caligiuri, Maureen
; APPLICANT: Nefsky, Bradley
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,205A
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSV-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 766 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-539-205A-4

Query Match 12.8%; Score 96.5; DB 3; Length 766;
Best Local Similarity 32.4%; Pred. No. 0.0088;
Matches 22; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy 6 LEVLLVGAKGLENTDYLCNMDPYAILKCRSQEQKSIATGKGTTPWNNFIPTVSDRTT 65
Db 10 IRVTIVAADGLYKRDVFRFPDFAVLTVDGEQTHHTTAIKKTLNPNWNETPEVNVTONST 69
Qy 66 DLVIKLM 73
Db 70 -IAIQVFD 76

RESULT 14
US-09-392-163A-4
; Sequence 4, Application US/09392163A
; Patent No. 6503742
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Caligiuri, Maureen
; APPLICANT: Nefsky, Bradley
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,163A
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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/539,205
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSV-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 766 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-392-163A-4

Query Match 12.8%; Score 96.5; DB 4; Length 766;
Best Local Similarity 32.4%; Pred. No. 0.0088;
Matches 22; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy 6 LEVLLVGAKGLENTDYLCNMDPYAILKCRSQEQKSIATGKGTTPWNNFIPTVSDRTT 65
Db 10 IRVTIVAADGLYKRDVFRFPDFAVLTVDGEQTHHTTAIKKTLNPNWNETPEVNVTONST 69
Qy 66 DLVIKLM 73
Db 70 -IAIQVFD 76

RESULT 15
US-09-538-092-853
; Sequence 853, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 853
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P05127
; US-09-538-092-853

Query Match 12.7%; Score 96; DB 4; Length 673;
Best Local Similarity 26.7%; Pred. No. 0.0084;
Matches 32; Conservative 17; Mismatches 47; Indels 24; Gaps 3;

Qy 6 LEVLLVGAKGLENTDYLCNMDPYAILKC-----RSQKSSKIATGKGTTPWNNFIPTV- 60
Db 173 LVLVRDAKNLVPMDFNGLSDPYVVKLIPDPKSESKQTKTKKSLNPNWNETFRFLK 232
Qy 61 -SDRTTDLVIKLMDSDTGADDFVGRATIFL-----BAVYTERSIPT 101
Db 233 ESDKRRRLSVEIWDNLTSRDNFNGSLSGFISLQKASVDGWFKLLSQSEGEYFNVVPP 292

Search completed: January 6, 2005, 14:04:17
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Job time : 43 secs

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2	756	100.0	177	15	US-10-425-114-379991	Sequence 379991,
3	605.5	80.1	144	16	US-10-437-963-198977	Sequence 198977,
4	574.5	76.0	144	17	US-10-425-115-337424	Sequence 337424,
5	523	69.2	155	15	US-10-425-114-60607	Sequence 60607,
6	496	65.6	242	17	US-10-425-115-351774	Sequence 351774,
7	482	63.8	151	16	US-10-437-963-144023	Sequence 144023,
8	465.5	61.6	136	16	US-10-767-701-42740	Sequence 42740,
9	465	61.5	144	17	US-10-425-115-196450	Sequence 196450,
10	485	61.5	144	17	US-10-425-115-291094	Sequence 291094,
11	460.5	60.9	143	17	US-10-425-115-196454	Sequence 196454,
12	455	60.2	167	16	US-10-437-963-189521	Sequence 189521,
13	437	56.5	141	17	US-10-425-115-307041	Sequence 307041,

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Db 121 TFTPEDTRQGLPEDFGWKQSS 143

RESULT 2
US-10-425-114-37991
; Sequence 37991, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37991
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-020-C12_FLI.pep
US-10-425-114-37991

Query Match 100.0%; Score 756; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMPPYAILKCRSQEQKSSATGKGTTPWNNENFIFTV 60
Db 35 MVHGTLEVLVGAAGLENTDYLNNMPPYAILKCRSQEQKSSATGKGTTPWNNENFIFTV 94
QY 61 SDRTTDLVIKLDSDTGTDADFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGKVKGL 120
Db 95 SDRTTDLVIKLDSDTGTDADFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGKVKGL 154
QY 121 TFTPEDTRQGLPEDFGWKQSS 143
Db 155 TFTPEDTRQGLPEDFGWKQSS 177

RESULT 3
US-10-437-963-198977
; Sequence 198977, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198977
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94586C.1.pep
US-10-437-963-198977
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Query Match 80.1%; Score 605.5; DB 16; Length 144;
Best Local Similarity 79.9%; Pred. No. 5.6e-59;
Matches 115; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMPPYAILKCRSQEQKSSATGKGTTPWNNENFIFTV 60
Db 1 MVQGTLEVLVGAAGLENTDYLNNMPPYAVLKCRSQEQKSSVASKGSDPEWNETPMFSV 60
QY 61 SDRTTDLVIKLDSDTGTDADFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGKVKGL 120
Db 61 THNATELIKLDSDSGTDDDFVGEATISLEAIYTEGSIPTPTVYVNVKDEYRGEIKVGL 120
QY 121 TFTPEDTRQGL-PEDFGWKQSS 143
Db 121 TFTPEDTRQGLSEEDIGWKQSS 144

RESULT 4
US-10-425-115-337424
; Sequence 337424, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337424
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70901C.1.pep
US-10-425-115-337424

Query Match 76.0%; Score 574.5; DB 17; Length 144;
Best Local Similarity 74.3%; Pred. No. 1.6e-55;
Matches 107; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMPPYAILKCRSQEQKSSATGKGTTPWNNENFIFTV 60
Db 1 MAQGTLEVLVGAAGLENTDYLNNMPPYAVLKCRSQEQKSTVASKGSDPEWNETPFVTV 60
QY 61 SDRTTDLVIKLDSDTGTDADFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGKVKGL 120
Db 61 SENATELVKLDSDGGTDDSVGEATIPDGVYTEGSIPTPTVYVNVKDEYRGEIKVGL 120
QY 121 TFTPEDTRQGLPED-FGWKQSS 143
Db 121 TFTPEDTRQGLPEENYGGWQSS 144

RESULT 5
US-10-425-114-60607
; Sequence 60607, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60607
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3597-068-All_FLI.pgp
US-10-425-114-60607

Query Match      69.2%; Score 523; DB 15; Length 155;
Best Local Similarity 78.6%; Pred. No. 9.3e-50;
Matches 99; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MVHGTLVLLVGAGLNTDYLGNMDDPYAILKCRSQEOKSSIAATGKTTPEWNNFIETV 60
Db 27 MAOQTLEVLVVGARGLENTDYLGNMDDPYAILKCRSQEOKSSVASKGCEPEWNETFVETV 86

Qy 61 SDRTTDLVILKMDSDTGTADDVFGAETIPLAAYVTERSIPPTLVNVVKGKCYGKIKVGL 120
Db 87 SDGNAELFIKLLDSDDGTTDDFVGEATIPLEAVYTEGNIPPTLVNVVVKDEYRGEIKVGL 146

Qy 121 TFTPED 126
Db 147 TFTPED 152

RESULT 6
US-10-425-115-351774
; Sequence 351774, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351774
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(242)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83984C.1.pgp
US-10-425-115-351774

Query Match      65.6%; Score 496; DB 17; Length 242;
Best Local Similarity 61.9%; Pred. No. 1.7e-46;
Matches 99; Conservative 11; Mismatches 16; Indels 34; Gaps 1;

Qy 1 MVHGTLVLLVGAGLNTDYLGNMDDPYAILKCRSQEOKSSIAATGKTTPEWNNFIETV 60
Db 80 MAOQTLEVLVVGARGLENTDYLGNMDDPYAILKCRSQEOKSSVASKGCEPEWNETFVETV 139

Qy 61 SDRTTDLVILKMDSDTGTADDVFGAETIPLAAYVTERSIPPTLVNVVKGKCYGKIKVGL 87
Db 140 SDGNAELFIKLLDSDDGTTDDFVGEATYXSLSSAYLSTSLVNSILHGLYQLLILVLS 199

Qy 88 -IPLAAYVTERSIPPTLVNVVKGKCYGKIKVGLTFTPED 126
Db 200 QIPLEAVYTEGNIPPTLVNVVVKDEYRGEIKVGLTFTPED 239

RESULT 7
US-10-437-963-144023
; Sequence 144023, Application US/10437963

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; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144023
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44875C.1.pep
US-10-437-963-144023

Query Match      63.8%; Score 482; DB 16; Length 151;
Best Local Similarity 62.7%; Pred. No. 3.2e-45;
Matches 94; Conservative 10; Mismatches 14; Indels 32; Gaps 1;

QY    25 MDPAYILKCSQBOKSSSIAT-----GKGTTPW 52
Db    1 MDPAYILKCSQBQRSSIASVLWCIADEWDLTVRIIPKECIAMCNFCVDCGKGSNPW 60

QY    53 NENFIFTSVRTDVLVIKLMSDTGTADDVFGEATIPLEAVYTTERSIPPTLYNVVKGEKY 112
Db    61 NENFVPSPDKATELLIKLASDTGSDPDDVFGEATIPLEPVYTEGSIPPLYNVVKDDHS 120

QY    113 CGEIKVGLTFTPEDTRORGLPEDFGGWKQS 142
Db    121 CGEIKVGLPFPEDVRORGLPEDFGGWKQS 150

RESULT 8
US-10-767-701-42740
; Sequence 42740, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42740
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C15003_1.pep
US-10-767-701-42740

Query Match      61.6%; Score 465.5; DB 16; Length 136;
Best Local Similarity 68.4%; Pred. No. 1.9e-43;
Matches 93; Conservative 15; Mismatches 23; Indels 5; Gaps 3;

QY    1 MVHGTLVLIVGAKGLENTDYLCNMDPYAILKCRSQEQKSSIATGKGTTPWNNFIPTV 60
Db    1 MVHGKLEVLIVSAGLEDTFDLNMDFVILTCTQEQKSSVANGSGSEPEWNETFIFTV 60

QY    61 SDRTTDLVIKLMSDTGTADDVFGEATIPLEAVYTTERSIPPTLYNVVKGEKYCGEIKVGL 120
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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60607
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3597-068-All_FLI.pgp
US-10-425-114-60607

Query Match      69.2%; Score 523; DB 15; Length 155;
Best Local Similarity 78.6%; Pred. No. 9.3e-50;
Matches 99; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MVHGTLVLLVGAGLNTDYLGNMDDPYAILKCRSQEOKSSIAATGKTTPEWNNFIETV 60
Db 27 MAOQTLEVLVVGARGLENTDYLGNMDDPYAILKCRSQEOKSSVASKGCEPEWNETFVETV 86

Qy 61 SDRTTDLVILKMDSDTGTADDVFGAETIPLAAYVTERSIPPTLVNVVKGKCYGKIKVGL 120
Db 87 SDGNAELFIKLLDSDDGTTDDFVGEATIPLEAVYTEGNIPPTLVNVVVKDEYRGEIKVGL 146

Qy 121 TFTPED 126
Db 147 TFTPED 152

RESULT 6
US-10-425-115-351774
; Sequence 351774, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351774
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(242)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83984C.1.pgp
US-10-425-115-351774

Query Match      65.6%; Score 496; DB 17; Length 242;
Best Local Similarity 61.9%; Pred. No. 1.7e-46;
Matches 99; Conservative 11; Mismatches 16; Indels 34; Gaps 1;

Qy 1 MVHGTLVLLVGAGLNTDYLGNMDDPYAILKCRSQEOKSSIAATGKTTPEWNNFIETV 60
Db 80 MAOQTLEVLVVGARGLENTDYLGNMDDPYAILKCRSQEOKSSVASKGCEPEWNETFVETV 139

Qy 61 SDRTTDLVILKMDSDTGTADDVFGAETIPLAAYVTERSIPPTLVNVVKGKCYGKIKVGL 87
Db 140 SDGNAELFIKLLDSDDGTTDDFVGEATYXSLSSAYLSTSLVNSILHGLYQLLILVLS 199

Qy 88 -IPLAAYVTERSIPPTLVNVVKGKCYGKIKVGLTFTPED 126
Db 200 QIPLEAVYTEGNIPPTLVNVVVKDEYRGEIKVGLTFTPED 239

RESULT 7
US-10-437-963-144023
; Sequence 144023, Application US/10437963

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Db 61 SDETPQLHLKIMSDV-TNDDFVGEATIPLEAVFQESLPPAVHPVVKKEKYCGEIKLAL 119
QY 121 TFTP-EDTRQGLPED 135
Db 120 TFTPAAETRHR---PDD 132
RESULT 9
US-10-425-115-196450
; Sequence 196450, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 196450
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_110748C.1.pep
US-10-425-115-196450
Query Match 61.5%; Score 465; DB 17; Length 144;
Best Local Similarity 63.7%; Pred. No. 2.3e-43;
Matches 93; Conservative 18; Mismatches 25; Indels 10; Gaps 4;
QY 1 MVHGTELVLLVGAKGLENTDYLNNMDPYAILKCRQEQKSSATGKTTPEWNEPIFTV 60
Db 1 MVHGKLEVLVSAGLEDTDFLNNMDPFVILTCRTQEQKSSVANGAGSEPEWNETFVFTV 60
QY 61 SDRTDLVIKLMDSDTGTADDVFGATIPLEAVYTERSIPTPLYNVVKGEKYCGEIKVGL 120
Db 61 SDDTPQLHLKIMSDL-TNDDFVGEATIPLEAVFQESLPPAVHPVVKKEKYCGEIKLAL 119
QY 121 TFTP-EDTRQGLPED-----FGW 139
Db 120 TFTPAAETRHR--PDDNEEGPPYSSW 143
RESULT 10
US-10-425-115-291094
; Sequence 291094, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 291094
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_28567C.1.pep
US-10-425-115-291094
Query Match 61.5%; Score 465; DB 17; Length 144;
Best Local Similarity 63.7%; Pred. No. 2.3e-43;
Matches 93; Conservative 18; Mismatches 25; Indels 10; Gaps 4;
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```
QY 1 MVHGTELVLLVGAKGLENTDYLNNMDPYAILKCRQEQKSSATGKTTPEWNEPIFTV 60
Db 1 MVHGKLEVLVSAGLEDTDFLNNMDPFVILTCRTQEQKSSVANGAGSEPEWNETFVFTV 60
QY 61 SDRTDLVIKLMDSDTGTADDVFGATIPLEAVYTERSIPTPLYNVVKGEKYCGEIKVGL 120
Db 61 SDDTPQLHLKIMSDL-TNDDFVGEATIPLEAVFQESLPPAVHPVVKKEKYCGEIKLAL 119
QY 121 TFTP-EDTRQGLPED-----FGW 139
Db 120 TFTPAAETRHR--PDDNEEGPPYSSW 143
RESULT 11
US-10-425-115-196454
; Sequence 196454, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 196454
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_110751C.1.pep
US-10-425-115-196454
Query Match 60.9%; Score 460.5; DB 17; Length 143;
Best Local Similarity 62.8%; Pred. No. 7.3e-43;
Matches 91; Conservative 18; Mismatches 27; Indels 9; Gaps 3;
QY 1 MVHGTELVLLVGAKGLENTDYLNNMDPYAILKCRQEQKSSATGKTTPEWNEPIFTV 60
Db 1 MVHGKLEVLVSAGLEDTDFLNNMDPFVILTCRTQEQKSSVANGAGSEPEWNETFVFTV 60
QY 61 SDRTDLVIKLMDSDTGTADDVFGATIPLEAVYTERSIPTPLYNVVKGEKYCGEIKVGL 120
Db 61 SDDTPQLHLKIMSDL-TNDDFVGEATIPLEAVFQESLPPAVHPVVKKEKYCGEIKLAL 119
QY 121 TFTP-EDTRQGLPED-----FGW 139
Db 120 TFTPAAETRHR--PDDNEEGPPYSSW 142
RESULT 12
US-10-437-963-189521
; Sequence 189521, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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; SEQ ID NO 189521
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86022C.1.pap
US-10-437-963-189521

Query Match      60.2%; Score 455; DB 16; Length 167;
Best Local Similarity 62.9%; Pred. No. 3.7e-42;
Matches 90; Conservative 15; Mismatches 26; Indels 12; Gaps 1;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MVHGKLEVLVCAKGLDTEFLNDMDPYVILTCRSEQSVAKGAGSEPEWNETFPFV 60

Qy 61 SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVL 120
Db 61 SDDVPQLNVKIMDSNADDFVGEANIPLEVPFLEGLPPPAVHRVVKBEKCYGKIKVAL 120

Qy 121 TFTP-----EDTRQG 131
Db 121 TFTPAAETRRHHNHNENEGTRTG 143

RESULT 13
US-10-425-115-307041
; Sequence 307041, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 307041
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_43093C.1.pap
US-10-425-115-307041

Query Match      56.5%; Score 427; DB 17; Length 141;
Best Local Similarity 56.6%; Pred. No. 3.8e-39;
Matches 81; Conservative 23; Mismatches 37; Indels 2; Gaps 1;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MVRGKLEVLVSAKGLDSDFFNSMDPYVILTCRSEQSVASGAGSEPEWNETFPFV 60

Qy 61 SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVL 120
Db 61 SGDAPELRVKIMDSALSDADLVGEACIPLEAVLQEGSLPPAVHRVVKDEYRGEIKIAL 120

Qy 121 TFTPEDTRQGLPEDFGWKQSS 143
Db 121 TFTPABENEE--ESYGMNQST 141

RESULT 14
US-10-425-114-46233
; Sequence 46233, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46233
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701130512_FLI.pap
US-10-425-114-46233

Query Match      53.5%; Score 404.5; DB 15; Length 149;
Best Local Similarity 52.1%; Pred. No. 1.3e-36;
Matches 76; Conservative 29; Mismatches 38; Indels 3; Gaps 1;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MPRGTLEVLVISARGIDDDNFLSSIDPVILTYRAQEKSTVQEDAGSKPQWNESEFLTV 60

Qy 61 SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVL 120
Db 61 SDSASELNLKIMDKDNFSQDDCLGEATIHLDPVFEAGSIPETAYKVVKDEYCCGEIKVAL 120

Qy 121 TFTPEDTRQGL---PEDFGWKQSS 143
Db 121 TFTAERNEEQYDAPBESYGMWKSS 146

RESULT 15
US-10-424-599-220600
; Sequence 220600, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 420600
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41232C.1.pap
US-10-424-599-220600

Query Match      39.7%; Score 300.5; DB 15; Length 153;
Best Local Similarity 42.5%; Pred. No. 4.9e-25;
Matches 65; Conservative 30; Mismatches 45; Indels 13; Gaps 4;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MAIGPWEVLVAKGLQETDIFAHMDPYVLLQYKQGERKSSVTHEGGRNFINWEKFFRV 60

Qy 61 ----SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGK 110
Db 61 EYPGSGDQYKLNLRIMDKDVFSDDFVQQTIVKOLLAEAGSALRPHKYSVVVRAD 120

Qy 111 K-YCGEIKVGLTFTPTDTRQGLPEDFGWKQS 142
Db 121 QSYCGEIEVGITFTRKE--EYIEDDVGGWKES 151
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Search completed: January 6, 2005, 14:15:34
Job time : 150 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 13:25:47 ; Search time 194 Seconds
(without alignments)
424.116 Million cell updates/sec

Title: US-09-913-569B-6

Perfect score: 756

Sequence: 1 MVHGTLEVLVAGKGLNTD.....PEDTRORGLPEDFGWKQS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt.02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	91.0	143	2 Q6H7E3	Q6H7E3 oryza sativ
2	605.5	80.1	144	2 Q82550	Q82550 oryza sativ
3	605.5	80.1	144	2 Q7F9X0	Q7F9X0 oryza sativ
4	605.5	80.1	144	2 CAE03867	CAE03867 oryza sat
5	486.5	64.4	147	2 Q9C886	Q9C886 arabidopsis
6	483.5	64.0	147	2 Q8LDR6	Q8LDR6 arabidopsis
7	455.5	60.3	143	2 Q24582	Q24582 zea mays (m
8	455	60.2	128	2 Q9SMH6	Q9SMH6 zea mays (m
9	454.5	60.1	145	2 Q7XPW6	Q7XPW6 oryza sativ
10	393.5	52.1	143	2 Q9ZRV6	Q9ZRV6 cicer ariet
11	259	34.3	156	2 Q50006	Q50006 oryza sativ
12	259	34.3	156	2 Q7GC09	Q7GC09 oryza sativ
13	247.5	32.7	159	2 Q8LPB3	Q8LPB3 oryza sativ
14	246.5	32.6	159	2 Q50005	Q50005 oryza sativ
15	240.5	31.8	156	2 Q9M2T2	Q9M2T2 arabidopsis
16	240.5	31.8	159	2 Q7Y021	Q7Y021 oryza sativ
17	232	30.7	151	2 Q8S2B8	Q8S2B8 oryza sativ
18	186	24.6	137	1 P16B_CUCMA	Q9ZT46 cucurbita m
19	179	23.7	254	2 Q9U7F0	Q9U7F0 eufolliculi
20	177	23.4	149	1 P16A_CUCMA	Q9ZT47 cucurbita m
21	166	22.0	247	2 Q945X9	Q945X9 arabidopsis
22	166	22.0	247	2 AA741866	AA741866 arabidops
23	155	20.5	595	2 Q9SDM4	Q9SDM4 dunaliella
24	151	20.0	953	2 Q7PTC2	Q7PTC2 anopheles g
25	149.5	19.8	1020	2 Q9ZVT9	Q9ZVT9 arabidopsis
26	146.5	19.4	221	2 Q6ES10	Q6ES10 oryza sativ
27	145	19.2	279	2 Q49490	Q49490 arabidopsis
28	139.5	18.5	575	2 Q7XTW4	Q7XTW4 oryza sativ
29	136.5	18.1	422	2 Q6U0U5	Q6U0U5 oryza sativ
30	136.5	18.1	422	2 AAQ56572	AAQ56572 oryza sat
31	136.5	18.1	565	2 Q6ZDC3	Q6ZDC3 oryza sativ

32 136.5 18.1 565 2 BAC92419 BAC92419 oryza sat
33 130 17.2 242 2 Q8T925 Q8T925 tetrahymena
34 129.5 17.1 528 2 Q9ZVY8 Q9ZVY8 arabidopsis
35 129.5 17.1 560 2 Q8L706 Q8L706 arabidopsis
36 129.5 17.1 574 2 Q9FY55 Q9FY55 arabidopsis
37 128.5 17.0 515 2 Q7XAL6 Q7XAL6 oryza sativ
38 125.5 16.6 306 2 Q8TAX2 Q8TAX2 homo sapien
39 125.5 16.6 466 2 Q9NUS2 Q9NUS2 homo sapien
40 125.5 16.6 863 2 Q7S1B8 Q7S1B8 neurospora
41 125.5 16.6 878 2 Q6DN12 Q6DN12 homo sapien
42 125 16.5 532 2 Q8LOF0 Q8LOF0 oryza sativ
43 125 16.5 538 2 Q6ETC4 Q6ETC4 oryza sativ
44 125 16.5 1081 2 Q6Z8U1 Q6Z8U1 oryza sativ
45 125 16.5 1081 2 BAD10009 BAD10009 oryza sat

ALIGNMENTS

RESULT 1

Q6H7E3 PRELIMINARY; PRT; 143 AA.
AC Q6H7E3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative elicitor-responsive gene-3.
GN Name=P0010C01.27;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: Contains 1 C2 domain.
DR EMBL: AP004768; BAD25356.1; -.
DR InterPro: IPR000008; C2_CaLB.
DR InterPro: IPR008973; C2_CaLB.
DR Pfam: PF00168; C2; 1.
DR PRINTS: PRO0360; C2DOMAIN.
DR SMART: SM00239; C2; 1.
DR PROSITE: PS00004; C2 DOMAIN 2; 1.
SQ SEQUENCE 143 AA; 15776 MW; B8256661199B3956 CRC64;

Query Match 91.0%; Score 688; DB 2; Length 143;

Best Local Similarity 89.4%; Pred. No. 7e-61;
Matches 127; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MVHGTLEVLVAGKGLNTDYLGNMDFYAILKCRSQSKSIATGKTTPWNNFIFTV 60
Db 1 MVHGTLEVLVAGKGLNTDYLGNMDFYAILKCRSQSKSIATGKTTPWNNFIFTV 60
Qy 61 SDRTDLVIKLMDSDTGADDFVGEATIPLEAVYTERSIPPTLYNVVKGYCIGKVL 120
Db 61 SDKATELLIKLDSDTGADDFVGEATIPLEAVYTERSIPPTLYNVVKDEHYCIGKVL 120

Qy 121 TPTPEDTRORGLPEDFGWKQS 142

Db 121 TPTPEDVRORGLPEDFGWKQS 142

RESULT 2

ID Q82550 PRELIMINARY; PRT; 144 AA.
AC Q82550
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Elicitor-responsive gene-3.
GN Name=ERG3;

Dd 61 SEGTTTELKAKIFDKXDVGTEDDAVGATIPLEBPVFVEGSIPTPAYNVVVKDEEYKGGEIWWAL

:
:
:
:

Qy 121 TFTPDPTRQRGLPED-FGGWKQS 142

Dd 121 SFKPSENRSRGWDEESYGWKS 143

RESULT 6
Q8LDR6 PRELIMINARY; PRT; 147 AA.
ID Q8LDR6 AC QBLDR6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBurel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBurel. 26, Last annotation update)
DE Putative elicitor-responsive gene.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsia.
NCBI_TaxID=3702;
OX NCBI TaxID=
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volfovsky N., Town C.D.; Troukhan M., Alexandrov N.,
FA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002) .
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RC Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AY085843; AAM63058.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CoLB.
DR Pfam; PF00168; C2_1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2_1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
SQ SEQUENCE 147 AA; 16194 MW; 8B051C9CAE22CA4B CRC64;

Query Match 64.0%; Score 483.5; DB 2; Length 147;
Best Local Similarity 65.0%; Pred. No. 2.3e+0;
Matches 93; Conservative 16; Mismatches 33; Indels 1; Gaps 1

Qy 1 MVHGTLVLIVGAGLGENTDYLCNMDDPYAILKCRSBOKSSIA TGKTTPENNETFI FTV 60
Db 1 MPHGTLEVLIWSAKGLEADPFNNMDPVQLTCR TDQGSNVAEGMTTPEWNETFIFTV 60
Qy 61 SDRTDLAVIKLMDS DTDADDVCGETAPLEA VYTERTSPITLYNNVVKGKYCGEKVGL 120
Db 61 SEGTTTELKAKIFDKXDVGTEDDAVGATIPLE BPVFVEGSIPTPAYNVVVKDEEYKGGEI WWAL 120

Qy 121 TFTPDPTRQRGLPED-FGGWKQS 142

Dd 121 SFKPSENRSRGWDEESYGWKS 143

RESULT 7
O24582 PRELIMINARY; PRT; 143 AA.
ID O24582 AC O24582;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBurel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBurel. 26, Last annotation update)
DE Novel protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI TaxID=4577;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OX euroside 1; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Etolated epicotyls;
RA Dupico B., Esteban R., Labrador E.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AJ012692; CAA10133.1; -.
DR HSSP; P05696; 1DSY.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KW Hypothetical protein
SQ SEQUENCE 143 AA; 16091 MW; 64ED12D3671B4732 CRC64;

Query Match 52.1%; Score 393.5; DB 2; Length 143;
Best Local Similarity 51.7%; Pred. No. 2.4e-31;
Matches 74; Conservative 27; Mismatches 39; Indels 3; Gaps 1;

QY 1 MHGTEVLVVGAKGLENLDYLCNMDPYAILKCRSQKSIATGKGTTPWNNFTV 60
Db 1 MPRGTLEVLLSAGLENDLFLSDIPYVILSYRAQEHKSTVQEGAGSNPQWNETFLFTV 60

QY 61 SDRTTDLVILKMDSDTGTADDFVGEATIPLEAVYTERSIPPTLYNNVKGKYL 120
Db 61 SDSASELRLRMKDNFNNDNLGEALIPLEAVFEGLAENAYKLKVEQYCGEIKVAL 120

QY 121 TPTPDRQGLPDPFGGWKQSS 143
Db 121 TPTPDRNDEE---ETCGGWKEST 140

RESULT 11
O50006 PRELIMINARY; PRT; 156 AA.
AC O50006;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Os-FIERG2 protein.
GN Name=Os-FIERG2;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.-Y., Choe M.S., Jeong S.-Y., Bae C.-G., Cheong Y.H., Han C.-D.,
RA Cho M.-J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 C2 domain.
DR EMBL; U951336; AAC04628.1; -.
DR PIR; T04363; T04363.
DR HSSP; P04410; 1A25.
DR Gramene; O50006; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ SEQUENCE 156 AA; 17436 MW; 63EAB8006CBA2D90 CRC64;

Query Match 34.3%; Score 259; DB 2; Length 156;
Best Local Similarity 41.3%; Pred. No. 8.1e-18;
Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;

QY 4 GTLEVLVVGAKGLENLDYLCNMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
Db 5 GVLEVLVDAKGLTGNDPLGKIDIPYVYVQYRSQKRSVARDQGNPSWNEVFKQINST 64

QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNNVKGK-Y 112
Db 65 AATGQHKLFURLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124

QY 113 CGEIKVGLTFTPTDRQGLPDPFGGWKQS 142
Db 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153

RESULT 12
O7GC09 PRELIMINARY; PRT; 156 AA.
AC O7GC09;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RPP17-2.
GN Name=Rpp17-2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22086689; PubMed=12091721;
RA Asano T., Kusano H., Okuda T., Kubo N., Shimada H., Kadowaki K.;
RA "Rpp16 and Rpp17, from a common origin, have different protein
RT characteristics but both genes are predominantly expressed in rice
RT phloem tissues";
RL Plant Cell Physiol. 43:668-674 (2002).
CC -I- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AB060730; BAC06446.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ SEQUENCE 156 AA; 17436 MW; 63EAB8006CBA2D90 CRC64;

Query Match 34.3%; Score 259; DB 2; Length 156;
Best Local Similarity 41.3%; Pred. No. 8.1e-18;
Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;

QY 4 GTLEVLVVGAKGLENLDYLCNMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
Db 5 GVLEVLVDAKGLTGNDPLGKIDIPYVYVQYRSQKRSVARDQGNPSWNEVFKQINST 64

QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNNVKGK-Y 112
Db 65 AATGQHKLFURLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124

QY 113 CGEIKVGLTFTPTDRQGLPDPFGGWKQS 142
Db 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153

RESULT 13
Q8LPB3 PRELIMINARY; PRT; 159 AA.
AC Q8LPB3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RPP17-1.
GN Name=Rpp17-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

QY 4 GTLEVLVVGAKGLENLDYLCNMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
Db 5 GVLEVLVDAKGLTGNDPLGKIDIPYVYVQYRSQKRSVARDQGNPSWNEVFKQINST 64

QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNNVKGK-Y 112
Db 65 AATGQHKLFURLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124

QY 113 CGEIKVGLTFTPTDRQGLPDPFGGWKQS 142
Db 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153

RESULT 12
O7GC09 PRELIMINARY; PRT; 156 AA.
AC O7GC09;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RPP17-2.
GN Name=Rpp17-2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22086689; PubMed=12091721;
RA Asano T., Kusano H., Okuda T., Kubo N., Shimada H., Kadowaki K.;
RA "Rpp16 and Rpp17, from a common origin, have different protein
RT characteristics but both genes are predominantly expressed in rice
RT phloem tissues";
RL Plant Cell Physiol. 43:668-674 (2002).
CC -I- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AB060730; BAC06446.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ SEQUENCE 156 AA; 17436 MW; 63EAB8006CBA2D90 CRC64;

Query Match 34.3%; Score 259; DB 2; Length 156;
Best Local Similarity 41.3%; Pred. No. 8.1e-18;
Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;

QY 4 GTLEVLVVGAKGLENLDYLCNMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
Db 5 GVLEVLVDAKGLTGNDPLGKIDIPYVYVQYRSQKRSVARDQGNPSWNEVFKQINST 64

QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNNVKGK-Y 112
Db 65 AATGQHKLFURLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124

QY 113 CGEIKVGLTFTPTDRQGLPDPFGGWKQS 142
Db 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153

RESULT 13
Q8LPB3 PRELIMINARY; PRT; 159 AA.
AC Q8LPB3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RPP17-1.
GN Name=Rpp17-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Search completed: January 6, 2005, 14:02:45
Job time : 198 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 07:53:54 ; Search time 4016 Seconds
(without alignments)
10315.183 Million cell updates/sec

Title: US-09-913-569B-5
Perfect score: 876
Sequence: 1 gcacgaggttcgttcacgcc.....ttttgtgatccttgaaaaa 876

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_bg.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358.4	40.9	827	8 AK120841	Oryza sat
2	291.6	33.3	760	8 AK063584	AK063584 Oryza sat
3	290.6	33.2	710	8 AF090598	AF090598 Oryza sat
4	276.8	31.6	432	6 BD178086	Novel pro
5	275.4	31.4	874	8 BT009547	BT009547 Triticum
6	247	28.2	247	11 BV081654	BV081654 scl239_p3
7	247	28.2	247	11 BV081655	BV081655 scl239_p3
8	247	28.2	247	11 BV109995	BV109995 PZA01487
9	247	28.2	247	11 BV109997	BV109997 PZA01487
10	246.4	28.1	248	11 BV081650	BV081650 scl239_p3
11	246.4	28.1	248	11 BV081657	BV081657 scl239_p3
12	246.4	28.1	248	11 BV109999	BV109999 PZA01487
13	246.4	28.1	248	11 BV110002	BV110002 PZA01487
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15	246	28.1	246	11 BV109993	BV109993 PZA01487
16	242	27.6	242	11 BV081651	BV081651 scl239_p3
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19	237.4	27.1	239	11 BV110000	BV110000 PZA01487

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21	236.8	27.0	240	11	BV109994
22	231	26.4	231	11	BV081656
23	231	26.4	231	11	BV109998
24	222	25.3	222	11	BV081649
25	222	25.3	222	11	BV110001
26	215.6	24.6	222	11	BV110003
27	198	22.6	198	11	BV110004
28	197.2	22.5	667	8	BT012761
29	194.8	22.2	699	8	AK070539
30	190.2	21.7	697	8	AY085843
31	190.2	21.7	726	8	AY054623
32	189.4	21.6	490	8	AY081504
33	178.6	20.4	695	8	BT009577
34	174.8	20.0	498	8	AF152601
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36	160	18.3	160	11	BV109996
37	153	17.5	655	8	CAR012692
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40	91	10.4	483	6	AX785024
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42	79.8	9.1	3713	8	AB060729
43	79.8	9.1	65190	2	BI011H02
44	79.8	9.1	140454	8	OSJN00183
45	73.4	8.4	860	8	BT009397

ALIGNMENTS

AK120841 827 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone: J02302G19, full insert sequence.

ACCESSION AK120841
VERSION AK120841.1 GI:37990464

KEYWORDS FLU CDNA; CAP trapper.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1

AUTHORS

The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team., Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group., Otono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Taunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Ikeda, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

JOURNAL MEDLINE 22752273

PUBMED 12869764

REFERENCE 2

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Inamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,

Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murasa, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Nariikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasato, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsato, N., Ota, Y., Otomo, Y., Ryu, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shiehiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Ikeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
 Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

3 (bases 1 to 827)
 Kikuchi, S.
 Direct Submission
 Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuch@nias.affrc.go.jp).
 Tel: 81-29-838-7007, Fax: 81-29-838-7007
 This clone is one of the 32K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Teunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oeato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaki-Akahara, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers

	Location/Qualifiers
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	/mol_type="mRNA"
	/cultivar="Nipponbare"
	/db_xref="taxon:39947"
	/clone="J023022G19"
ORIGIN	
Query Match	40.9%; Score 358.4; DB 8;
Best Local Similarity	85.0% ; Pred. No. 4.7e-88;
Matches 401; Conservative	0; Mismatches 71; Indels 0; Gaps 0;
Qy	30 GCACAGGGGTCTTGCGGAGCAGCGAGGCCGAGGAGGCATGGTCCACGGACCGTTGG 89
Dd	54 CGCGAGCAGCGCGGCAAGGAGGAAGAGGAGGAGGAGGAGTAGTGTCACGGCACGTTGG 113

Qy	90	AAGTGTGCTCGTTGGGGCCAAAGGGCTCTGAGAACACCGATTACCTCTGTAAACATGGATC	149
Db	114	AGGTGTGCTCGTTCGGGGCCAAAGGGCTCTGAGAACACCGATTACCTGTGTCAACATGGATC	173
Qy	150	CGTATGCAATTCATCAAGTGCCTTCACAGAGCAGAGAGACGACGATTTGCAACTGGAAAAG	209
Db	174	CATATGCATTCATCAAGTGCCTTCACAGAGCAGAGAGACGACGACGATTCAGGCNAAG	233
Qy	210	GAATCACTCCCTGAGTGGAAATGAAAACTTTATCTTCACTGTGTCTGACCGGACAAACAGACT	269
Db	234	GGAGTAACCCCTGAATGGAACGAAATCTTTGTCTTCCCGTGTCTGACAAAGCTACAGAGC	293
Qy	270	TGTTAATCAAGCTTTATGGACAGTGATACAGGCACAGCAGATGACTTTGTTGGTGAAGCAA	329
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Qy	390	TGAAAGGTGAAAAATACTCGGGGGAAATCAAAGTGTGCTCTCACATTCACCTCTCGAGATA	449
Db	414	TGAAGGATGAACTTCTGTGGAGAAATCAAAGTCGGCTCACATTCACCTCTCGAGATG	473
Qy	450	CTCCGACGCGGTCTCCGACAGGACTTCGGTGGATGGGAAGCAATCATCTTA	501
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AK063584			
LOCUS		760 bp	mRNA
DEFINITION		Oryza sativa (japonica cultivar-group)	cdNA clone:001-118-A01, full insert sequence.
ACCESSION		AK063584	
VERSION		AK063584.1	GI:32973602
KEYWORDS		FLU_CDNA; oligo-capping	
SOURCE		Oryza sativa (japonica cultivar-group)	
ORGANISM		Oryza sativa (japonica cultivar-group)	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	
AUTHORS		The Rice Full-Length cdNA Consortium, National Institute of	

Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi,S., Sacho,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,M., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuka,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Otono,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurotaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Miikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., KIKEN,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Haehidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
Japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
REFERENCE 12869764
AUTHORS 2 (bases 1 to 760)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hangaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kawaguchi,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,

Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kuroaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Oka, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takehashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kuroaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oka, Y., Saitoh, K., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sagaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

COMMENT

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

TITLE
JOURNAL

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Db 247 AACGAAACCTTTATGTTCAGCGTCACTCAACAACGCTCAGAGCTCATCATCAAGTTGATG 306
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Qy 519 GGTGCACACAGACAGCAGCAATTCATGCGCTTGGAGCCTTCAGC 564
Db 547 GTGCACTGCATCGCTATGCTAGTCTGCTGGAAGCCTGGAC 592

RESULT 3
AF090698 710 bp mRNA linear PLN 16-SEP-1998
LOCUS Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA, complete cds.
DEFINITION AF090698
ACCESSION AF090698
VERSION AF090698.1 GI:3603472
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 710)
Kim, C.Y., Cheon, S.Y., and Cho, M.J.
Identification and Characterization of Fungal Elicitor Responsive
Rice Genes by mRNA Differential Display
Unpublished
2 (bases 1 to 710)
Kim, C.Y., Cheon, S.Y., and Cho, M.J.
Direct Submission
Submitted (04-SEP-1998) Department of Biochemistry, PMBRC, 900
Gaja-dong, Chinha, Kyongnam 660-701, Republic of Korea

FEATURES
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Matches 394; Conservative 0; Mismatches 124; Indels 8; Gaps 2;
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Qy 107 GCCAAGGGCTCGAGAACACCGATTACTCTGTAACTGGATCCGATGCAATTCCTCAAG 166
Db 127 GCCAAGGGCTCGAGAACACCGACTACTCTGTGCAACATGGACCGGTACCGGTTCTCAA 186
Qy 167 TGGCGTTACAGGAGCAGAGCAGATTCGCACTGGAAAGAACTACCCCTGATGG 226
Db 187 TGGCGCTCGCAGGAGCAGAGCAGCGTTTCGTCAGGTAAAGATCTGACCCCTGAATGG 246

ORIGIN

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Best Local Similarity 74.9%; Pred. No. 3e-69;
Matches 393; Conservative 0; Mismatches 124; Indels 8; Gaps 2;

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Oy 214 TACCCCTGAGTGAATGAACCTTTATCTTCACCTGTGTCTGACCGGACACAGACTTGGT 273
Db 322 TGATCTGAGTGAAGCAACCTTTGTGTTCCCGTCTCTGAGAACTGAGCTTGT 381
Oy 274 AATCAAGCTTATGGACAGTGATACAGGCACAGCAGATGACTTTTGTGTGAAGCAACGAT 333
Db 382 CATCAAGCTACTGGACAGTGTATGTTGGTGGCAGCGACAGCAGCGTGTGTGAAGCAACGAT 441
Oy 334 TCCATTGGAACAGTGTATCTGAAGAGGAGATTCACCAACACTCTATATATTTGTGA 393
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Oy 394 AGGTGAAAATACTCGGGGAAATCAAAAGTTGGTCTCACATTCCTCTGAGGATCTCG 453
Db 502 AGACGAAGATGACGTGGAGAAATCAAAATTTGGTCTGACGTTCTCTCGGAGGAGCTCG 561
Oy 454 CCAGCGGGGTCTCCAGAGG---ACTTCGGTGGATGGAAGCAATCATCTTAGAGCTAGAT 510
Db 562 TGATCAGGATCAACCCGAGGAAACTATGTTGGTGGGAGGAACTCAATCATCTTGAGAAG 621
Oy 511 GCTTTAAGGGTCCACGAGCACAGCGCAAAATTCATGCGCTTGA 555
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LOCUS scl239_p3 Mol7 Zea mays Mol7 Zea mays STS genomic, sequence tagged
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ACCESSION BV081654.1 GI:37053311
VERSION BV081655.1
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCG
Primer B: AGTATTACTGGCTACACCTCCCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 72 81 75 77 74 81 79 68 65 63 57 59 54
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Best Local Similarity 100.0%; Pred. No. 3.3e-57;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 514 TTAAGGGTGCACGAGCAGCAGCAATTCATCGCTTGGAGCTTCAGCGCTCGAGTA 573
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Db 61 CTTTCATGCTAATGCAGAAATTCATTCGATTTGGCTTCTTTTGTATGTTTTCAGAAAGTGT 120
Oy 634 TATTAGTGAAGTTTCAACAAAATAGCTCCATATGCTCTATATCCCGTATTGGAATTC 693
Db 121 TATTAGTGAAGTTTCAACAAAATAGCTCCATATGCTCTATATCCCGTATTGGAATTC 180
Oy 694 TAAGCCGTTTGTGATTACTGCTTACACAGAGATTTGCTTCTAGTTCCTACCTACGCT 753
Db 181 TAAGCCGTTTGTGATTACTGCTTACACAGAGATTTGCTTCTAGTTCCTACCTACGCT 240
Oy 754 TTTTITTT 760
Db 241 TTTTITTT 247

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ACCESSION BV081655.1 GI:37053312
VERSION BV081655.1
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCG
Primer B: AGTATTACTGGCTACACCTCCCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM

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dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 35 46 42 42 39 35 39 34 30 30 32 32 58
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Query Match 28.2%; Score 247; DB 11; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.3e-57;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 TTTAAGGGTGCCACGACGACGACCAATTCATGCGCTTGGAGCCTTCAGCCGTCGAGT 572
Db 1 TTTAAGGGTGCCACGACGACGACCAATTCATGCGCTTGGAGCCTTCAGCCGTCGAGT 60

QY 573 ACTTCATGCTAATGCGAATTCATTCGATTGCGCTTCTTTGATTGTTTCAGAGAAGTG 632
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QY 693 CTAAGCCGTTTGTGATTACTGCTTACACAGAAGTTTGTCTTCTAGTTCACCTACGC 752
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QY 753 TTTTTTT 759
Db 241 TTTTTTT 247

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ACCESSION BV109995
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KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vron Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)
```

COMMENT

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCCC
STS size: 247
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 72 81 75 77 74 81 79 68 65 63 57 59 54
54 55 56 55 67 67 62 52 62 57 62 82 82 88 82 76 64 63 59 72 86
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source

/note="Organ: leaf; genomic DNA from inbred line"

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ORIGIN

Query Match 28.2%; Score 247; DB 11; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.3e-57;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 TTAAGGGTGCCACGACGACGACCAATTCATGCGCTTGGAGCCTTCAGCCGTCGAGTA 573
Db 1 TTAAGGGTGCCACGACGACGACCAATTCATGCGCTTGGAGCCTTCAGCCGTCGAGTA 60

QY 574 CTTTCATGCTAATGCGAATTCATTCGATTGCGCTTCTTTGATTGTTTCAGAGAAGTGT 633
Db 61 CTTTCATGCTAATGCGAATTCATTCGATTGCGCTTCTTTGATTGTTTCAGAGAAGTGT 120

QY 634 TATTAGTAGTTTCAACAAAAATAGCTCCATATTGCTCTATATCCGCTATTGGAATTC 693
Db 121 TATTAGTAGTTTCAACAAAAATAGCTCCATATTGCTCTATATCCGCTATTGGAATTC 180

QY 694 TAAGCCGTTTGTGATTACTGCTTACACAGAAGTTTGTCTTCTAGTTCACCTACGCT 753
Db 181 TAAGCCGTTTGTGATTACTGCTTACACAGAAGTTTGTCTTCTAGTTCACCTACGCT 240


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OY 754 TTTT TTTT 760
Db 241 TTTT TTTT 247

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ACCESSION BV109997
VERSION BV109997.1 GI:45427618
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SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACTCTCGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCGC
STS size: 247
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
PHRED/PHRAP Quality Scores 35 46 42 42 39 35 39 34 30 30 32 32 58
49 49 47 51 63 70 62 78 56 57 56 65 62 82 81 81 75 72 61 64 59
61 68 71 71 63 68 64 57 56 73 61 64 52 62 51 59 66 60 70 65 73 55
40 37 37 30 30 30 51 51 40 45 55 66 66 72 72 71 71 62 59 59 77 69
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ORIGIN

Query Match 28.2%; Score 247; DB 11; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.3e-57;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 513 TTTAAGGGTGCCAGAGCACAGCAATTCATGCGCTTGAGCGCTTCAGCCGTCGAGT 572
Db 1 TTTAAGGGTGCCAGAGCACAGCAATTCATGCGCTTGAGCGCTTCAGCCGTCGAGT 60

OY 573 ACTTCATGCTTAATGCAGAAATTCATTCGATTTGGCTTCTTTTTCATGTTTCAGAAAGT 632
Db 61 ACTTCATGCTTAATGCAGAAATTCATTCGATTTGGCTTCTTTTTCAGAAAGT 120

OY 633 TTATTAGTGTAGTTTCAACAAAAATAGCTCCATATTCCTATATCCGTTATTCGAAAT 692
Db 121 TTATTAGTGTAGTTTCAACAAAAATAGCTCCATATTCCTATATCCGTTATTCGAAAT 180

OY 693 CTAAGGCCGTTTGTGATTACTGCTTACAACAAGATTTTTCCTTCTAGTTCCTACTAGC 752
Db 181 CTAAGGCCGTTTGTGATTACTGCTTACAACAAGATTTTTCCTTCTAGTTCCTACTAGC 240

OY 753 TTTT TTTT 759
Db 241 TTTT TTTT 247

RESULT 10
BV081650
LOCUS
DEFINITION scl239 p3 Kull1 Zea mays Kull1 Zea mays STS genomic, sequence tagged site.
ACCESSION BV081650
VERSION BV081650.1 GI:37053307
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 248)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACTCTCGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCGC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
PHRED/PHRAP Quality Scores 35 46 42 42 39 35 39 34 30 30 32 32 58
49 49 47 51 63 70 62 78 56 57 56 65 62 82 81 81 75 72 61 64 59
61 68 71 71 63 68 64 57 56 73 61 64 52 62 51 59 66 60 70 65 73 55
40 37 37 30 30 30 51 51 40 45 55 66 66 72 72 71 71 62 59 59 77 69
76 76 71 66 66 82 88 85 86 86 84 80 77 69 69 64 63 63 66 82 88 90
90 89 82 82 80 69 70 65 65 60 68 86 90 72 69 70 61 60 63 68 73
67 69 68 72 60 64 64 76 73 90 78 84 76 76 85 90 90 90 88 81
74 73 80 80 80 80 80 82 89 87 83 74 71 71 71 76 73 80 80 89 89
77 80 74 80 74 68 50 50 50 56 56 44 44 44 44 43 43 42 73 66 70
74 83 74 71 74 78 79 76 75 67 61 59 64 70 43 43 42 42 43 40 31
31 31 37 37 37 37 40 40 56 56 56 56 56 56 56 44 56 56 56 42 42
42 42 40 51 51 51 51 56 56 56 48 48 36.
Location/Qualifiers
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Ky21"
/db_xref="taxon:4577"
/clone_lib="Zea mays Ky21"
/dev_stages="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<l. .>247

Contact: Brandon S. Gaut
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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTGC
Primer B: AGTATTACTGGCTACACCTCCCC
STS size: 248
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 81 67 76 76 76 75 78 72 67 60 61 61 55
55 52 57 58 56 62 65 52 61 58 65 62 76 65 71 73 84 78 77 71 67 82
88 80 81 75 73 76 61 63 58 71 63 63 59 64 52 54 56 61 66 60 62 54
59 58 66 55 55 74 79 75 66 57 57 82 87 90 90 89 90 65 37 40
40 40 27 27 45 40 56 56 90 88 82 74 70 68 69 69 77 90 90
90 89 85 85 84 77 68 58 58 66 71 79 77 69 77 62 61 61 77 77
73 75 73 66 66 68 69 80 75 75 76 76 71 80 90 90 90 90 90 88
88 85 83 86 77 77 84 76 71 80 79 73 71 81 75 86 84 90 90
81 81 76 76 72 87 90 90 87 87 74 74 69 80 75 81 75 72 78
74 89 78 69 78 80 78 81 81 74 62 62 66 78 76 84 79 76 81 75 85
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/clone_lib="Zea mays Hp301"
/dev_stages="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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ORIGIN
Query Match 28.1%; Score 246.4; DB 11; Length 248;
Best Local Similarity 99.6%; Pred. No. 4.9e-57;
Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 513 TTTAAGGCTGACAGAGCAGGACAAATTCATCGCTTGGAGCTTCAGCCGTCGAGT 572
Db 1 TTTAAGGCTGACAGAGCAGGACAAATTCATCGCTTGGAGCTTCAGCCGTCGAGT 60
Qy 573 ACTTCATGCTAATCAGAAATTCATTCGATTTGGCTTCTTTTGATTTGTTTCAGAGAAAGTG 632
Db 61 ACTTCATGCTAATCAGAAATTCATTCGATTTGGCTTCTTTTGATTTGTTTCAGAGAAAGTG 120
Qy 633 TTATTAGTGGTTTCAACAAAAATAGCTCCATATTCGTCTATATCCGTTATTCGAAATT 692
Db 121 TTATTAGTGGTTTCAACAAAAATAGCTCCATATTCGTCTATATCCGTTATTCGAAATT 180
Qy 693 CTAAGGCCGTTTGATTTACTGCTTACAAAGAAATTTTCTCTAGTTCCCACTACGC 752
Db 181 CTAAGGCCGTTTGATTTACTGCTTACAAAGAAATTTTCTCTAGTTCCCACTACGC 240
Qy 753 TTTTITTTT 760

Db 241 TTTTITTTT 248

RESULT 13
BV110002
LOCUS
DEFINITION
PZA01487 Kull1 Zea mays Kull1 Zea mays STS genomic, sequence tagged site.
ACCESSION
BV110002
VERSION
BV110002.1
KEYWORDS
GI:45427623
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 248)
McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTGC
Primer B: AGTATTACTGGCTACACCTCCCC
STS size: 248
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 90 86 90 90 76 76 83 79 66 61 61 61 61
63 61 63 70 69 83 84 79 79 76 77 77 77 83 90 90 90 90 89 89 87
90 87 88 82 82 73 70 60 60 78 78 78 78 66 66 71 78 79 90 90 86
86 79 87 84 89 89 89 82 82 65 68 62 79 90 90 90 89 84 90 84
83 88 77 71 82 88 90 88 90 87 83 82 82 85 90 90 90 90
90 90 90 90 72 75 72 72 87 90 77 77 74 77 75 90 90
85 82 77 78 79 79 87 90 90 88 86 86 86 90 90 90 87 87
84 85 90 90 90 90 90 90 90 90 84 84 84 89 85 90 90 90
90 90 81 81 90 90 90 90 74 74 75 89 89 90 89 86 86
84 90 89 85 90 90 90 90 82 78 78 86 79 82 81 80 77 77 90
90 90 72 70 70 69 64 42 43 44 44 55 55 56 56 56 56 56
44 56 56 56 56 56 56 56 56 56 56 56 N.

FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="Kull1"
/db_xref="taxon:4577"
/clone_lib="Zea mays Kull1"
/dev_stages="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..248

source

ORIGIN

Query Match 28.1%; Score 246.4; DB 11; Length 248;
Best Local Similarity 99.6%; Pred. No. 4.9e-57;
Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 513 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 572
DB 1 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 60

QY 573 ACTTCATGCTAATGCGAGAATTCATGCTGCTTCTTTGATGCTTTTCAGAGAAGTG 632
DB 61 ACTTCATGCTAATGAGAATTCATGCTGCTTCTTTGATGCTTTTCAGAGAAGTG 120

QY 633 TTATTAGTGTGTTTCAACAAAAATAGCTCCATATTCATGCTCTATATCCCGTATTGGAAAT 692
DB 121 TTATTAGTGTGTTTCAACAAAAATAGCTCCATATTCATGCTCTATATCCCGTATTGGAAAT 180

QY 693 CTAAGCCGTTTGTGATTTACTGCTTACAAAGAAGTTTGTCTTCTAGTTCCCACTACGC 752
DB 181 CTAAGCCGTTTGTGATTTACTGCTTACAAAGAAGTTTGTCTTCTAGTTCCCACTACGC 240

QY 753 TTTTITTTT 760
DB 241 TTTTITTTT 248

RESULT 14
BV081652
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BV081652 246 bp DNA linear STS 30-SBP-2003
sc1239_p3 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
site.

BV081652 1 GI:37053309
BV081652 STS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
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REFERENCE
AUTHORS
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COMMENT

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Dept., Ecology and Evolutionary Biology
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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATCTCGC
Primer B: AGTATTACTGGCTTACACTCTCCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 89 90 84 84 84 82 87 79 73 66 52 50 50
51 51 53 56 51 67 67 57 66 55 57 60 76 67 72 80 80 83 70 66 61 63

FEATURES
source

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40 35 39 24 24 24 46 46 37 29 29 40 43 40 39 22 22 35 43
46 51 72 61 61 77 Location/Qualifiers
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/db_xref="taxon:4577"
/clone_lib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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Query Match 28.1%; Score 246; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 572
DB 1 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 60

QY 573 ACTTCATGCTAATGCGAGAATTCATTCGATTTGGCTTCTTTTGTGTTTCAGAAGAAGTG 632
DB 61 ACTTCATGCTAATGCGAGAATTCATTCGATTTGGCTTCTTTTGTGTTTCAGAAGAAGTG 120

QY 633 TTATTAGTGTGTTTCAACAAAAATAGCTCCATATTCATGCTCTATATCCCGTATTGGAAAT 692
DB 121 TTATTAGTGTGTTTCAACAAAAATAGCTCCATATTCATGCTCTATATCCCGTATTGGAAAT 180

QY 693 CTAAGCCGTTTGTGATTTACTGCTTACAAAGAAGTTTGTCTTCTAGTTCCCACTACGC 752
DB 181 CTAAGCCGTTTGTGATTTACTGCTTACAAAGAAGTTTGTCTTCTAGTTCCCACTACGC 240

QY 753 TTTTITTTT 758
DB 241 TTTTITTTT 246

RESULT 15
BV109993
LOCUS

BV109993 246 bp DNA linear STS 13-MAR-2004
PZA01487 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
site.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BV109993
BV109993.1 GI:45427614
BV109993 STS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Brandon S. Gaut
Dept., Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATCTCGC
Primer B: AGTATTACTGGCTTACACTCTCCC
STS size: 246
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 89 90 84 84 84 82 87 79 73 66 52 50 50
51 51 53 56 51 67 67 57 66 55 57 60 76 67 72 80 80 83 70 66 61 63
70 64 84 70 66 72 56 56 63 71 76 71 77 63 65 65 81 83 69 64 55
40 35 39 24 24 46 46 37 37 29 29 40 43 40 39 22 22 22 35 43
46 51 72 61 61 77 80 86 79 85 90 85 82 72 70 65 65 65 66 88 90 90
90 87 87 85 85 79 73 61 56 56 72 79 69 63 65 58 54 54 61 69
67 66 60 60 55 62 63 77 87 90 79 75 72 79 90 90 90 90 86 75
75 65 67 79 79 79 73 85 84 74 71 71 60 71 73 73 89 89
86 86 74 75 75 71 44 44 44 48 48 28 28 44 44 44 74 77 75
74 77 66 61 42 42 42 48 32 32 32 44 44 44 76 72 71 77 72 68 68
72 76 70 62 61 65 66 51 51 42 42 46 42 42 42 44 44 44 42 47
47 56 47 56 47 47 47 47 48 48 48 48 48.

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/molecule="genomic DNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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ORIGIN

Query Match 28.1%; Score 246; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 513 TTTAAGGGTGACACAGACAGACAGCAATTCATCGCGCTTCGAGCCTTCAGCCGTCGAGT 572
Db 1 TTTAAGGGTGACACAGACAGACAGCAATTCATCGCGCTTCGAGCCTTCAGCCGTCGAGT 60
Qy 573 ACTTCATGCTAATGCAGAAATTCATCGAAATTTGGCTTCTTTTGGATTGTTTCAGAGAAGTG 632
Db 61 ACTTCATGCTAATGCAGAAATTCATCGAAATTTGGCTTCTTTTGGATTGTTTCAGAGAAGTG 120
Qy 633 TTATTAGTGAGTTTCAACAAAAATAGCTCCATATTCCTCTATATCCGTAATTCGAAAT 692
Db 121 TTATTAGTGAGTTTCAACAAAAATAGCTCCATATTCCTCTATATCCGTAATTCGAAAT 180
Qy 693 CTAAGGCGGTTTGATTTACTGCTTACAAAGAAAGTTTTCCTTCTAGTCCCACTACGC 752
Db 181 CTAAGGCGGTTTGATTTACTGCTTACAAAGAAAGTTTTCCTTCTAGTCCCACTACGC 240
Qy 753 TTTTTT 758
Db 241 TTTTTT 246

Search completed: January 8, 2005, 10:24:44
Job time : 4018 secs

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CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 876 BP; 241 A; 176 C; 226 G; 233 T; 0 U; 0 Other;

Query Match 100.0%; Score 876; DB 3; Length 876;
Best Local Similarity 100.0%; Pred. No. 6e-261;
Matches 876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACGAGGTTGCTTACGCGCACAGGCAAGGCGCTGTGAGGGAGCGAGGAGC 60
DB 1 GCACGAGGTTGCTTACGCGCACAGGCAAGGCGCTGTGAGGGAGCGAGGAGC 60
QY 61 GGAGGAGCATGGTGCACGGGACGCTGGAAGTGTCTGTTGGGGCCCAAGGGCTCGA 120
DB 61 GGAGGAGCATGGTGCACGGGACGCTGGAAGTGTCTGTTGGGGCCCAAGGGCTCGA 120
QY 121 GAACACGATTACCTCTGTAACATGATCGTATGCAATTCCTCAAGTGCCTTACAGGA 180
DB 121 GAACACGATTACCTCTGTAACATGATCGTATGCAATTCCTCAAGTGCCTTACAGGA 180
QY 181 GCAGAGAGCAGTATTGCAACTCGAAAGAACTACCCCTGAGTGGAAATGAAACCTTAT 240
DB 181 GCAGAGAGCAGTATTGCAACTCGAAAGAACTACCCCTGAGTGGAAATGAAACCTTAT 240
QY 241 CTTCACTGTCTGACGGGACACAGACTTGGTAATCAAGCTTATGACAGTGATACAGG 300
DB 241 CTTCACTGTCTGACGGGACACAGACTTGGTAATCAAGCTTATGACAGTGATACAGG 300
QY 301 CACAGCAGATGACTTGTGCTGGAAGCAAGTTCATTTGGAAGCAGTGTATCTCAAG 360
DB 301 CACAGCAGATGACTTGTGCTGGAAGCAAGTTCATTTGGAAGCAGTGTATCTCAAG 360
QY 361 GAGCATTTCACCAACTCTATTAATGTTGGAAGGTGAAATAATCTGCGGGGAAATCAA 420
DB 361 GAGCATTTCACCAACTCTATTAATGTTGGAAGGTGAAATAATCTGCGGGGAAATCAA 420
QY 421 AGTTGCTCTCATTCACTCTGAGNATCTCCGACGGGGCTCCGAGGACCTCG 480
DB 421 AGTTGCTCTCATTCACTCTGAGNATCTCCGACGGGGCTCCGAGGACCTCG 480
QY 481 TGGATGGAAGCAATCATCTTAGAGTAGATGCTTTAAGGTGCACAGAGCACAGCGACA 540
DB 481 TGGATGGAAGCAATCATCTTAGAGTAGATGCTTTAAGGTGCACAGAGCACAGCGACA 540
QY 541 ATTCAATCGGTTGGAGCCTTCAGCCGTCGAGTACTTCATGCTAATGAGAAATTCATCGA 600
DB 541 ATTCAATCGGTTGGAGCCTTCAGCCGTCGAGTACTTCATGCTAATGAGAAATTCATCGA 600
QY 601 TTTGGCTCTCTTGTATGTTTCAGAAAGTGTATTAGTGTTCACCAAAAATAGC 660
DB 601 TTTGGCTCTCTTGTATGTTTCAGAAAGTGTATTAGTGTTCACCAAAAATAGC 660
QY 661 TCCATATTGCTCTATATCCCGTATTGAAATTTCTAAGGCCGTTTGTGATTACTGCTTACA 720
DB 661 TCCATATTGCTCTATATCCCGTATTGAAATTTCTAAGGCCGTTTGTGATTACTGCTTACA 720
QY 721 ACAAGAAGTTTGTCTTCTAGTTCCTACTACGCTTTTTTTTGAAGTGTGAGTGAACATC 780
DB 721 ACAAGAAGTTTGTCTTCTAGTTCCTACTACGCTTTTTTTTGAAGTGTGAGTGAACATC 780
QY 781 TTTGTGTTCAACGTTTGGGAGGTGTAGGCCAGTAACTACGAAAGAAATTAATTTCC 840
DB 781 TTTGTGTTCAACGTTTGGGAGGTGTAGGCCAGTAACTACGAAAGAAATTAATTTCC 840
QY 841 CTTGACGCAACATTGTTTTTTTGTGATCCTTTGAAAAA 876

DB 841 CTTGACGCAACATTGTTTTTTTGTGATCCTTTGAAAAA 876

RESULT 2
AAC79365
ID AAC79365 standard; cDNA; 544 BP.

XX AAC79365;

XX 06-FEB-2001 (first entry)

XX Plant viral movement protein encoding cDNA SEQ ID 35.

XX Plant viral movement protein; transport; transgenic plant;

XX Viral resistance; cosuppression; ss.

XX Zea mays.

XX WO200060088-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009110.

XX 07-APR-1999; 99US-0128092P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Krebbers E, Weng Z, Cahoon RE;

XX WPI; 2000-638467/61.

XX P-PSDB; AAB44511.

XX Novel viral movement polypeptides and polynucleotides useful in field of
XX plant molecular biology, for producing transgenic plants, to prepare
XX antibodies and in immunological screening of cDNA expression libraries.

XX Disclosure; Page 53; 62pp; English.

XX Polynucleotide sequences AAC79348-C79375 encode plant viral movement
XX proteins AAB4494-B44520. Some plant viruses have been shown to be able
XX to establish systemic infections via movement proteins that utilize
XX existing plant pathways to traffic macromolecules to surrounding cells.
XX Proteins such as those of the invention are similar to viral movement
XX proteins that function in the transport of nucleic acids from cell to
XX cell. The plant viral movement proteins are useful for obtaining a
XX nucleic acid fragment encoding a viral movement protein. Polynucleotides
XX encoding the plant viral movement proteins are useful for positive
XX selection of a transformed cell. The proteins are useful in the field of
XX plant molecular biology, and in the preparation of antibodies against the
XX proteins. The proteins are also useful for isolating cDNAs and genes
XX encoding homologous proteins from the same or other plant species, and to
XX create transgenic plants in which the protein is presented at higher or
XX lower levels than normal or in cell types or developmental stages in
XX which they are not normally found. The proteins and nucleotide sequences
XX may be used to control cosuppression and engineer plant virus resistance

XX Sequence 544 BP; 154 A; 120 C; 144 G; 118 T; 0 U; 8 Other;

Query Match 50.2%; Score 440; DB 3; Length 544;
Best Local Similarity 96.4%; Pred. No. 1.1e-125;
Matches 460; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 8 GTTCGTTACGCCACAGGCAAGGCGCTGTGAGGGAGAGCGAGCGAGGAG 67

DB 1 GTTCGTTACGCCACAGGCAAGGCGCTGTGAGGGAGAGCGAGCGAGGAG 60

QY 68 GACATGGTGCACGGGACGCTGGAAGTGTCTGTTGGGGCCCAAGGGCTTCGAGAACACC 127

DB 61 GACATGGTGCACGGGACGCTGGAAGTGTCTGTTGGGGCCCAAGGGCTTCGAGAACACC 120

QY 128 GATTACCTCTGTAACATGGATCCGATCGCAATTCCTCAAGTCCGTTTCACAGGAGCAGAG 187

Db 121 GATTACCTCTGTAAACATGGATCCGTATGCAATTTCTCAAGTGCCGTTTCACAGGACGAGAAG 180
Qy 188 AGCAGTATTGCAACTGGAAGAAAGAACTACCCCTCAGTGGGAATGAAACTTTTATCTTCACT 247
Db 181 AGCAGTATTGCAACTGGAAGAAAGAACTACCCCTCAGTGGGAATGAAACTTTTATCTTCACT 240
Qy 248 GTGCTGACCGGACACAGACTTGGTAAATCAAGCTTATGGACAGTGATACAGGCACAGCA 307
Db 241 GTGCTGACCGGACACAGACTTGGTAAATCAAGCTTATGGACAGTGATACAGGCACAGCA 300
Qy 308 GATGACTTTGTTGGTGAAGCAACGATTCCATTGGAAGCAGTGATATCTGAAAGAGCAATT 367
Db 301 GATGACTTTGTTGGTGAAGCAACGATTCCATTGGAAGCAGTGATATCTGAAAGAGCAATT 360
Qy 368 CCACCAACACTCTATAATGTTGTAAGGTGAAAGAACTACGCGGGGAAATCAAAAGTTGGT 427
Db 361 CCACCAACACTCTATAATGTTGTAAGGTGAAAGAACTACGCGGGGAAATCAAA-NTGGT 419
Qy 428 CTCACATTCACTCTGAGGATACCTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGGA 484
Db 420 CTCACATTCACTCTGAGGATACCTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGTGA 476

RESULT 3

ADCS3921
ID ADCS3921 standard; DNA; 432 BP.

XX AC ADCS3921;

XX DT 18-DEC-2003 (first entry)

XX DE DNA encoding rice phloem protein of the invention #1.

XX KW Rice; ds; gene; phloem protein; Ca2+/phospholipid-combining domain;
XX KW promoter; transgenic plant; phloem-specific; exotic protein;
XX KW virus MP-like gene.

XX OS Oryza sativa.

XX FH Key Location/Qualifiers

FT CDS 1. .432
FT /tag= a
FT /product= "phloem protein #1"
FT /transl_except= (pos:61..63,aa:Trp)
FT /transl_except= (pos:82..84,aa:Trp)
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FT /transl_except= (pos:310..312,aa:Trp)
FT /transl_except= (pos:334..336,aa:Trp)

XX PN JP2002315582-A.

XX PD 29-OCT-2002.

XX XX 24-APR-2001; 2001JP-00126682.

XX XX 24-APR-2001; 2001JP-00126682.

XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX DR WPI; 2003-407228/39.

XX DR P-PSDB; ADCS3922.

XX PT A new protein in rice phloem and its gene, a DNA, a promoter, a
XX PT transgenic plant.

XX PS Claim 8; SEQ ID NO 1; 18pp; Japanese.

XX CC The invention discloses a rice phloem protein having Ca2+/phospholipid-
XX CC combining domain. Also claimed is a DNA encoding the novel rice phloem
XX CC protein, a promoter comprising a 1288 or 1572 base pair sequence, given
XX CC in the specification, a transgenic plant transformed to express phloem-
XX CC specifically the novel rice phloem protein, preparation of the novel rice

CC phloem protein by using the transgenic plant, a transgenic plant which
CC produces, phloem-specifically, an exotic protein. The method is used for
CC producing an exotic protein specifically in the phloem of a plant. The
CC gene represents a new virus MP-like gene from rice. The sequence
CC presented is a DNA encoding a rice phloem protein of the invention.

XX SQ Sequence 432 BP; 122 A; 93 C; 124 G; 93 T; 0 U; 0 Other;

Query Match 31.6%; Score 276.8; DB 10; Length 432;

Best Local Similarity 79.2%; Pred. No. 4.8e-75;

Matches 342; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

Qy 71 ATGTGTGACGGGACGCTGGAAGTGTCTGCTGTGGGGCCAAAGGCCCTCGAGAAACCCGAT 130

Db 1 ATGTGTGACGGGACGCTGGAAGTGTCTGCTGTGGGGCCAAAGGCCCTCGAGAAACCCGAC 60

Qy 131 TACTCTGTAACATGGATCCGTATGCAATTTCTCAAGTCCGTTTCACAGGACGAGAAGGC 190

Db 61 TACTCTGTAACATGGATCCGTATGCAATTTCTCAAGTCCGTTTCACAGGACGAGAAGGC 120

Qy 191 AGTATTGCAACTCGGAAAGGAACCTACCCCTGAGTGGAAATGAAAACCTTTATCTTCACTGTG 250

Db 121 AGGTTGCGTCAGGTAAGGATCTGACCCCTGAATGGAAACGAAACCTTTATGTTGAGCGTC 180

Qy 251 TCTGACCGGACAAACAGACTTTGGTAAATCAAGCTTATGGACAGTGATACAGGCACAGCAGAT 310

Db 181 ACTCACAACGCTACAGAGCTCATCATCAAGTTGATGGACAGTGACAGTGGCAGCGATGAT 240

Qy 311 GACTTTGTTGGTGAAGCAACGATTCATCCCTGAGTGGAAATGAAAACCTTTATCTTCACTGTG 370

Db 241 GATTTTGTGGAGAAGCAACGATTTCTTTTGGAAAGCAATCTATACAGAAGGAAGCATACCC 300

Qy 371 CCAACACTCTATAATGTTGTAAGGTGAAAAGTAACTCGCGGGAAATCAAAAGTTGGTCTC 430

Db 301 CCAACTGTTTATAATGTTGTAAGGTGAAAAGTAACTCGCGGGAAATCAAAAGTTGGTCTG 360

Qy 431 ACATTCACTCTCAGGATACCTCGCCAGCGGGGTCTCCAGAG---GACTTCGGTGGATGG 487

Db 361 ACGTTCACTCCAGAGGATGATCGGATCGGGGTTTATCTGAGGAAGACATTTGGTGGATGG 420

Qy 488 AAGCAATCATCT 499

Db 421 AAGCAGTCATCT 432

RESULT 4

AAC79352

ID AAC79352 standard; cDNA; 874 BP.

XX AC AAC79352;

XX DT 06-FEB-2001 (first entry)

XX DE Plant viral movement protein encoding cDNA SEQ ID 9.

XX XX Plant viral movement protein; transport; transgenic plant;

XX KW viral resistance; cosuppression; ss.

XX OS Triticum aestivum.

XX PN WO200060088-A2.

XX PD 12-OCT-2000.

XX XX 06-APR-2000; 2000WO-US009110.

XX PR 07-APR-1999; 99US-0128092P.

XX XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX PA Krebbers E, Weng Z, Cahoon RE;

XX XX WPI; 2000-638467/61.

XX DR

DR	P-PSDB; AAB44498.	AC	AAC79349;
XX		XX	
PT	Novel viral movement polypeptides and polynucleotides useful in field of	DT	06-FEB-2001 (first entry)
PT	plant molecular biology, for producing transgenic plants, to prepare	XX	
PT	antibodies and in immunological screening of cDNA expression libraries.	DE	Plant viral movement protein encoding cDNA SEQ ID 3.
XX		XX	
PS	Claim 2; Page 38; 62pp; English.	KW	Plant viral movement protein; transport; transgenic plant;
XX		KW	viral resistance; cosuppression; se.
XX		XX	
CC	Polynucleotide sequences AAC79348-C79375 encode plant viral movement	OS	Zea mays.
CC	proteins AAB44494-B44520. Some plant viruses have been shown to be able	XX	
CC	to establish systemic infections via movement proteins that utilize	PN	WO200060088-A2.
CC	existing plant pathways to traffic macromolecules to surrounding cells.	XX	
CC	Proteins such as those of the invention are similar to viral movement	PD	12-OCT-2000.
CC	proteins that function in the transport of nucleic acids from cell to	XX	
CC	cell. The plant viral movement proteins are useful for obtaining a	XX	
CC	nucleic acid fragment encoding a viral movement protein. Polynucleotides	PF	06-APR-2000; 2000MO-US009110.
CC	encoding the plant viral movement proteins are useful for positive	XX	
CC	selection of a transformed cell. The proteins are useful in the field of	PR	07-APR-1999; 99US-0128092P.
CC	plant molecular biology, and in the preparation of antibodies against the	XX	
CC	proteins. The proteins are also useful for isolating cDNAs and genes	PA	(DUPO) DU PONT DE NEMOURS & CO E I.
CC	encoding homologous proteins from the same or other plant species, and to	XX	
CC	create transgenic plants in which the protein is presented at higher or	PI	Krebbers E, Weng Z, Cahoon RE;
CC	lower levels than normal or in cell types or developmental stages in	XX	
CC	which they are not normally found. The proteins and nucleotide sequences	XX	
CC	may be used to control cosuppression and engineer plant virus resistance	DR	WPI; 2000-638467/61.
XX		DR	P-PSDB; AAB44495.
SQ	Sequence 874 BP; 261 A; 188 C; 223 G; 202 T; 0 U; 0 Other;	XX	
	Query Match 31.4%; Score 275.4; DB 3; Length 874;		
	Best Local Similarity 71.6%; Pred. No. 1.9e-74;		
	Matches 376; Conservative 0; Mismatches 146; Indels 3; Gaps 1;		
Qy	34 AGGGGCTTGTGAGGAGAGCGAGAGCGGAGGAGGACATGGTGCACGGGACGCTGGAAGT 93	CC	Polynucleotide sequences AAC79348-C79375 encode plant viral movement
Db	142 AGCGGAGAGGAGGCGAGATCAGCGCGGAGAGAGATGGCGAGGGGACGCTGGAGT 201	CC	proteins AAB44494-B44520. Some plant viruses have been shown to be able
Qy	94 GCTCTCTGTTGGGCGGAGGCTCGAGACACCGATTACTCTGTAAACATGATCCGTA 153	CC	to establish systemic infections via movement proteins that utilize
Db	202 GCTCTCTGTTGGGCGGAGGCTCGAGACACCGATTACTCTGTAAACATGATCCGTA 261	CC	existing plant pathways to traffic macromolecules to surrounding cells.
Qy	154 TGCAATTTCTCAAGTCCGCTTTCACAGGAGCAGAGAGCAGTATTGCACTGGAAAAGAAC 213	CC	Proteins such as those of the invention are similar to viral movement
Db	262 CGCGTTCTAAATGCACCTCGCAGGAGGAGCAAGACCGTCTCTGAAAAGGAAG 321	CC	proteins that function in the transport of nucleic acids from cell to
Qy	214 TACCCCTGAGTGAATGAATACTTTATCTTCACTGTGTCTGACCGGACACAGCTTGT 273	CC	cell. The plant viral movement proteins are useful for obtaining a
Db	322 TGATCTGAGTGAACGAACCTTTGTGTTTCAACCGTCTCTGAGAAATGCAACTGAGCTGT 381	CC	nucleic acid fragment encoding a viral movement protein. Polynucleotides
Qy	274 AATCAAGCTTATGGACAGTGATACAGGCACAGCAGATGACTTTGTTGTTGAAGCAACGAT 333	CC	encoding the plant viral movement proteins are useful for positive
Db	382 CATCAAGCTACTGGACAGTGATGTGGCAGCAGCAGCAGCGTTGTTGAGNACGAT 441	CC	selection of a transformed cell. The proteins are useful in the field of
Qy	334 TCCATTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCAACCTCTATATGTTGTA 393	CC	plant molecular biology, and in the preparation of antibodies against the
Db	442 CCCATTGATGAGTGTACACTGAAGGAAGCATCCCACTGTTTACAAATGTTGTCAA 501	CC	proteins. The proteins are also useful for isolating cDNAs and genes
Qy	394 AGGTGAAAATACTCGGGGAAATCAAGTTGGTCTCACATTCATCTCTGAGGATCTCG 453	CC	encoding homologous proteins from the same or other plant species, and to
Db	502 AGACGAAGAGTACCGTGAGAAATCAAAATTTGGTCTGACGTTCACTCCGGAGGAGCTCG 561	CC	create transgenic plants in which the protein is presented at higher or
Qy	454 CCAGCGGGGTCTCCAGAGG---ACTTCGGTGGATGGAAGCAATCATCTTTAGAGCTAGAT 510	CC	lower levels than normal or in cell types or developmental stages in
Db	562 TGATCAGATCAACCCGAGGAAATATGTTGGTGGGAGAACCAATCATCTTTGAGAAGAAGC 621	CC	which they are not normally found. The proteins and nucleotide sequences
Qy	511 GCTTTAAGGGTGACACGAGCAGCAGCAATTCATGCGCTTGA 555	CC	may be used to control cosuppression and engineer plant virus resistance
Db	622 AGGTGCTTTGTGAACATGATGGTGCCTGACAAGTCGTGTGTAGAA 666		
RESULT 5			
AAC79349			
ID AAC79349 standard; cDNA; 916 BP.			
XX			

455 TGACGGTGGCACTGATGACGATTTTGTGGTGGAGCAACGATTCCTCTGGAGCAGTTTA 514
352 TACTGAAAGGAGCATTCCACCAACACTCTATAATCTTGTGAAAGTGAAAAATACTGCGG 411
515 CACGGNAGGAACATCCCTCCGACTGTTTACATGTTGTGAAGCAGGAAGTAACCGCGG 574
412 GGAATCAAAAGTTGGTCTTCACATTCACATTCCTGAGGA 447
575 AGAATCAAAAGTTGGCCTCAGCTTCACTCCAGAGGA 610

RESULT 6

ADJ39772
ID ADJ39772 standard; cDNA; 442 BP.

AC ADJ39772;

XX 06-MAY-2004 (first entry)

DE Plant cDNA #772.

XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.

OS Eukaryota.

XX US2004016025-A1.

XX 22-JAN-2004.

XX 26-SEP-2002; 2002US-00260238.

XX 26-SEP-2001; 2001US-0325277P.

XX 26-SEP-2001; 2001US-0325448P.

XX 04-APR-2002; 2002US-0370620P.

XX (BUDW/) BUDWORTH P.

XX (MOU/) MOUGHAMER T.

XX (BRIG/) BRIGGS S P.

XX (COOP/) COOPER B.

XX (GLAZ/) GLAZEROOK J.

XX (GOFF/) GOFF S A.

XX (KATA/) KATAGIRI F.

XX (KREP/) KREPS J.

XX (PROV/) PROVART N.

XX (RICK/) RICHE D.

XX (ZHUT/) ZHU T.

XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

XX Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;

XX WPI; 2004-190374/18.

XX New rice promoter, useful for manipulating crop plants to alter or

XX improve phenotypic characteristics, e.g. produce large quantities of oil

XX or proteins, resistance to insecticides, virus or fungi, stress tolerance

XX or high nutritional value.

CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 442 BP; 125 A; 97 C; 111 G; 109 T; 0 U; 0 Other;

Query Match 26.0%; Score 228; DB 12; Length 442;

Best Local Similarity 78.6%; Pred. No. 6.9e-60;

Matches 330; Conservative 0; Mismatches 45; Indels 45; Gaps 3;

Qy 71 ATGGTGACGGGACGCTGGAAGTCTCTGCTGGGGCCCAAGGCCCTCGAGAACCCGAT 130

Db 1 ATGGTGACGGGACGCTGGAAGTCTCTGCTGGGGCCCAAGGCCCTCGAGAACCCGAT 60

Qy 131 TACCTCTGT-----AACATGGA 147

Db 61 TACCTGTGTACGCATCAGCTTATAATCTTAAAGCGCATTTGCTTGAACATGGA 120

Qy 148 TCCGTATGCAATCTCAAGTGCCGTTCCAGGAGCAGAGCAGTATTGCAAC-TGGAA 206

Db 121 TCCATATGCAATCTCAAGTGCCGTTCCAGGAGCAGAGCAGTATTGCAAC-TGGAA 180

Qy 207 AAGGAACCTCCCTGAGTGAATGAAATTTTACCTTCTGCTGTGACCGGCAACAG 266

Db 181 AAGGAAGTAAACCTGATGAAGCAAACTTTGCTTCCCGTCTGACAAAGCTACAG 240

Qy 267 ACTTGTGTAATCAAGCTTATGACAGTATACAGCAGCAGCAGATGCTTTGTTGTTGAG 326

Db 241 AGCTGTTGATCAAGCTCTTGACAGTATGATCTGCTCAGCGGACGACTTTGTTGTTGAG 300

Qy 327 CAACGATTCCATTGGAAGCAGTGTATCTGAAAGGAGCATTCCACCAACACTCTATATG 386

Db 301 CAAC-ATTCCTTTGGAAGCAGTGTATCTGAAAGGAGTATTCACCAACTCTGTATATG 359

Qy 387 TTGTGAAAGTGAAAAATCTGCGGGGAAATCAAAGTTGGTCTCACAATTCCTCTGAGG 446

Db 360 TTGTGAAAGTGAAACATTACTGTGGAGAAATCAAAGTCCGCTCACAATTCCTCTGAGG 419

RESULT 7

AAD54388

ID AAD54388 standard; DNA; 683 BP.

XX AC AAD54388;

XX 17-JUN-2003 (first entry)

XX Lolium perenne elicitor-responsive protein a2 (LpEra2) DNA.

XX Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;

XX elicitor-responsive protein; disease resistance; plant defence response;

XX protein storage; pest resistance; genetic marker; gene therapy; antipept;

XX agricultural; LpEra2; ds.

OS Lolium perenne.

XX WO200288359-A1.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-AU000539.

XX 02-MAY-2001; 2001AU-00004735.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

PA (AGRE-) AGRESEARCH LTD.

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XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
PI WPI; 2003-201227/19.
XX
XX New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
XX Claim 5; Fig 18; 195pp; English.
XX
XX The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era2
CC (LpEra2) DNA
XX
XX Sequence 683 BP; 180 A; 175 C; 183 G; 143 T; 0 U; 2 Other;
SQ
Query Match 25.8%; Score 226.2; DB 8; Length 683;
Best Local Similarity 70.3%; Pred. No. 3.2e-59;
Matches 303; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 63 AGGAGGACATGTGCGACGGGACGCTGGAAGTGTCTGCTGGGGCCAAAGGCGCTCGAGA 122
DB |||||
223 AGAAGATGGCGCAGGCGCGGACGCTCGAGGTGCTGCTCGGAGCGCAAGGGGCTCGAGA 282
QY 123 ACACCGATTACCTCTGTACATGATGATCCGTATGCAATTTCTCAAGTCCGCTTCACAGGAGC 182
DB |||||
283 ACACCGACTACCTGTGCAACATGATGATCCCTACGCTTCTCAGAGTCACCTCCAATGAGC 342
QY 183 AGAAGAGCAGTATTGCAACTGGAAGAAAGGAACTACCCCTGAGTGGAAATGAAAATCTTTATCT 242
DB |||||
343 AGAGGAGCTCCGTTGCAGGAGGCAAGGAAGTGAAGCGGAGTGAACGAACTTTGTGT 402
QY 243 TCACCTGTGCTGACCGGACCAAGACTTGGTAATCAAGCTTATGGAAGTGAATGAAAGGCA 302
DB |||||
403 TCACGACCTCCGAAAACGCAACGAGCTCTGCAATCAAGCTCTCGGACGACGCAATGGAA 462
QY 303 CACGAGATGATTTGTTGGTGAAGCAACGATTCATGGAAGTGAAGTGAAGTGAAGTGAAG 362
DB |||||
463 CCAACGACGACGATGTTGGTGAAGCAAGGATCCCTCTGGATGCTGTCTATCTGAAAGGAA 522
QY 363 GCATTCACCAACACATCTATAATGTTGTGAAGGTGAAGAAATCTCGGGGAAATCAAAG 422
DB |||||
523 GCATACCAACCAACGTTTACATGTTGTCAAGATGAGTACTGTGGGAATCAGAA 582
QY 423 TTGGTCTCAATTCATCTCGAGGATCTCGCGGGGGTCTCCAGAGGAGCTTCGGTG 482
DB |||||
583 TTGGTCTCAAGTTCACTCCGAGGAGCTTACCATTATTTACCCGAGGAAATCTTCGGTG 642
QY 483 GATGGAAGCAA 493
DB |||||
643 GGTGGAGACAA 653
RESULT 8
AAD54387
ID AAD54387 standard; DNA; 707 BP.
XX
AC AAD54387;
XX
17-JUN-2003 (first entry)
XX
XX Lolium perenne elicitor-responsive protein al (LpEra1) DNA.
XX
XX Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
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KW protein storage; pest resistance; genetic marker; gene therapy; antipest;
KW agricultural; LpEra1; ds.
XX
XX Lolium perenne.
XX
XX WO200288359-A1.
XX
XX 07-NOV-2002.
XX
XX 01-MAY-2002; 2002WO-AU000539.
XX
XX 02-MAY-2001; 2001AU-00004735.
XX
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX (AGRE-) AGRESEARCH LTD.
XX
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX WPI; 2003-201227/19.
XX
XX New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
XX Claim 5; Fig 18; 195pp; English.
XX
XX The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era1
CC (LpEra1) DNA
XX
XX Sequence 707 BP; 185 A; 162 C; 179 G; 171 T; 0 U; 10 Other;
SQ
Query Match 25.8%; Score 226.2; DB 8; Length 707;
Best Local Similarity 70.3%; Pred. No. 3.2e-59;
Matches 303; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 63 AGGAGGACATGTGCGACGGGACGCTGGAAGTGTCTGCTGGGGCCAAAGGCGCTCGAGA 122
DB |||||
102 AGAAGATGGCGCAGGCGCGGACGCTCGAGGTGCTGCTCGGAGCGCAAGGGGCTCGAGA 161
QY 123 ACACCGATTACCTCTGTAAACATGATGATCCGTATGCAATTTCTCAAGTGCCTTCACAGGAGC 182
DB |||||
162 ACACCGACTACCTGTGCAACATGATCCCTACGCTTCTCAGAGTCACCTCCAATGAGC 221
QY 183 AGAAGAGCAGTATTGCAACTGGAAGAAAGGAACTACCCCTGAGTGGAAATGAAAATCTTTATCT 242
DB |||||
222 AGAGAGCTCCGTTGCGAAGGAAAGGAGTGAAGCGGAAATGGAACGAAATCTTTGTGT 281
QY 243 TCACCTGTGCTGACCGGACCAAGACTTGGTAATCAAGCTTATGGAAGTGAATGAAAGGCA 302
DB |||||
282 TCACGACCTCCGAAAACGCAACGAGCTCTGATCAAGCTCTGAGCAGCAGCAATGGAA 341
QY 303 CACGAGATGATTTGTTGGTGAAGCAACGATTCATGGAAGCAAGTGAATGATGATGAAAGGA 362
DB |||||
342 CCAACGACGACGATGTTGGTGAAGCAAGGATCCCTCTGGATGCTGTCTATCTGAAAGGAA 401
QY 363 GCATTCACCAACACATCTATAATGTTGTGAAGGTGAAGAAATCTCGGGGAAATCAAAG 422
DB |||||
402 GCATACCAACCAACAGTTTACATGTTGTCAAGATGAGAGTACTGTGGAGAAATCAGAA 461
QY 423 TTGGTCTCAATTCATCTCGAGGATCTCGCGGGGGTCTCCAGAGGAGCTTCGGTG 482
DB |||||
462 TTGGTCTCAAGTTCACTCCGAGGAGGCTTACCATTATTTACCCGAGGAAATCTTCGGTG 521
QY 483 GATGGAAGCAA 493
DB |||||
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Db 522 GGTGAGACAA 532

RESULT 9
AADS4386
ID AAD54386 standard; DNA; 828 BP.
XX
AC AAD54386;
XX
DT 17-JUN-2003 (first entry)
XX
DE Lolium perenne elicitor-responsive protein a (LpEra) DNA.
XX
KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DBF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
KW protein storage; pest resistance; genetic marker; gene therapy; antipept;
KW agricultural; LpEra; gene; ds.
XX
OS Lolium perenne.
XX
FH Key Location/Qualifiers
FT CDS 228..665
FT /*tag= a
FT /product= "Ryegrass Era (LpEra) protein"
XX
PN WO200288359-A1.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-AU000539.
XX
PR 02-MAY-2001; 2001AU-00004735.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2003-201227/19.
DR P-PSDB; AAE35936.
XX
PT New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
PS Claim 5; Fig 16; 195pp; English.
XX
CC The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
CC DNA
XX
SQ Sequence 828 BP; 214 A; 199 C; 203 G; 198 T; 0 U; 14 Other;

Query Match 25.8%; Score 226.2; DB 8; Length 828;
Best Local Similarity 70.3%; Pred. No. 3.5e-59;
Matches 303; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 63 AGAGGACATGTCACGGACGTCGGAAGTCGTCTGTTGGGCCCAAGGGCTCGAGA 122
|||
Db 223 AGAAGATGGCGCAGCGCGACGCTCGAGGTGCTCGTCGGAGCCCAAGGGCTCGAGA 282
|||
QY 123 ACACCGATTACCTCTGTAACATGATCCGTATGCAATTCCTCAAGTCGCTCACAGGAC 182
|||
Db 283 ACACCGACTACCTGTGCAACATGATCCCTACGGCTTCTCAGAGTCACCTCAATGAGC 342
|||
QY 183 AGAAGACAGTATTGCAACTGGAAAGGAACCTACCCCTGAGTGAATGAAAACCTTTATCT 242
|||

Db 343 AGAGGAGCTCGTTTCAGAAAGGCAAGAGTGAAGCCGAATGGAACGAAACCTTTGTGT 402
|||
QY 243 TCACTGTGTCTGACCGGACACAGACTTGGTAATCAAGCTTATGGACAGTATACAGCA 302
|||
Db 403 TCAGACCTTCGAAAAACGCAACCGAGCTCTGCATCAAGCTCCTGGACGACCAATGAA 462
|||
QY 303 CAGCAGATGACTTTTGGTGAAGCAACGATTCCATTGGAAGCAGTGTATATCTGAAAGGA 362
|||
Db 463 CCAACGACGACGATGTTGGTGAAGCAAGGATCCCTCTGGATGCTCTATATCTGAAGAA 522
|||
QY 363 GCATTCCACCACTCTATAATTTGTTGAAAGTGAAATACTCGGGGAAATCAAG 422
|||
Db 523 GCATACCACCAACAGTTTACAATTTGTCAAAGATGAAGAGTACTGTGGAGAAATCAGAA 582
|||
QY 423 TTGTCCTCACATTCACCTCCTGAGGATACCTGCCAGCGGGTCTCCAGAGGACTTCGGTG 482
|||
Db 583 TTGTCCTCAAGTTTCACTCCGAGGAGGCTTACCATTATTACCCGAGGAAAACCTTCGGTG 642
|||

483 GATGGAAGCAA 493
|||
Db 643 GGTGAGACAA 653
|||

RESULT 10
AADS4408
ID AAD54408 standard; cDNA; 1110 BP.
XX
AC AAD54408;
XX
DT 17-JUN-2003 (first entry)
XX
DE Lolium perenne elicitor-responsive protein a (LpEra) cDNA.
XX
KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DBF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
KW protein storage; pest resistance; genetic marker; gene therapy; antipept;
KW agricultural; LpEra; gene; ss.
XX
OS Lolium perenne.
XX
FH Key Location/Qualifiers
FT CDS 326..712
FT /*tag= a
FT /product= "Ryegrass Era (LpEra) protein"
XX
PN WO200288359-A1.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-AU000539.
XX
PR 02-MAY-2001; 2001AU-00004735.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2003-201227/19.
DR P-PSDB; AAE35945.
XX
PT New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
PS Claim 5; Fig 49; 195pp; English.
XX
CC The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in a
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
CC DNA
XX

CC and/or pest resistance, plant defence response and/or protein storage in
 CC plants. The nucleotide sequence information and/or single nucleotide
 CC polymorphisms of the nucleic acid are useful as genetic markers. They are
 CC also useful in gene therapy. The present sequence is ryegrass Era (UpEra)
 CC cDNA
 XX
 SQ Sequence 1110 BP; 322 A; 258 C; 275 G; 255 T; 0 U; 0 Other;

Query Match 25.6%; Score 224.6; DB 8; Length 1110;
 Best Local Similarity 70.1%; Pred. No. 1.3e-58;
 Matches 302; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
 QY 63 AGGAGGACATGTTGACGAGGAGCTGGAAGTCTGCTGTTGGGCAAGGCGCTCGAGA 122
 Db 321 AGAGATGGCGAGGCGGAGCGCTCGAGTGTCTGCTCGGAGCCAAAGGGCTCGAGA 380
 QY 123 ACACCGATTACCTCTCTTAACATGGATCCGATGTCGCAATTTCTCAAGTCCCGTTACAGGAGC 182
 Db 381 ACACCGACTACCTGTGCAACATGGATCCCTAGCGCTTCTCAGAGTCACCTCAATGAGC 440
 QY 183 AGAAGAGCAGTATTGCAACTGGAAGAACTACCCCTGAGTGGATGAAATCTTATCT 242
 Db 441 AGAGGAGCTCCGTTGACAGAGGCAAGGAAGTGAAGCGAATGGAACGAACCTTTGTGT 500
 QY 243 TCACTGTGTGACCGGACACAGACTTGTATCAAGCTTTATGGACAGTGTATACAGGCA 302
 Db 501 TCAGGACCTCCGAAACGACCGAGCTCTGCATCAAGCTCTGGACGACGCAATGGAA 560
 QY 303 CAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGA 362
 Db 561 CCAACGACGACGATGTTGGTGAAGCAAGGATCCCTCTGGATGCTGTCTATATGAAGAA 620
 QY 363 GCATTCACCAACACTCTATATGTTGTGAAGGTGAAATACTCCGGGGAAATCAAG 422
 Db 621 GCATACCAACCAAGTTTACATATGTTGTCAAGATGAAGAGTACTGTGGAGAAATCAGAA 680
 QY 423 TTGGTCTCATTCTACTCTGAGGATACCTCGCCAGCGGGTCTCCAGAGGACTTCGGTG 482
 Db 681 TTGGTCTCAAGTTCACTTCGGAGGAGCTTAGCATTTATTACCCGAGGAAATCTCGGTG 740
 QY 483 GATGGAAGCA 493
 Db 741 GGTGGAGACAA 751

RESULT 11
 AAC79364
 ID AAC79364 standard; cDNA; 617 BP.
 AC AAC79364;
 XX
 DT 06-FEB-2001 (first entry)
 XX
 DE Plant viral movement protein encoding cDNA SEQ ID 33.
 XX
 KW Plant viral movement protein; transport; transgenic plant;
 XX viral resistance; cosuppression; ss.
 KW
 XX Zea mays.
 OS
 XX WO200060088-A2.
 PN
 XX 12-OCT-2000.
 PD
 XX
 PF 06-APR-2000; 2000WO-US009110.
 XX
 PR 07-APR-1999; 99US-0128092P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Krebbers E, Weng Z, Cahoon RE;
 XX
 XX WPI; 2000-638467/61.
 DR

DR P-PSDB; AAB44510.
 XX Novel viral movement polypeptides and polynucleotides useful in field of
 PT plant molecular biology, for producing transgenic plants, to prepare
 PT antibodies and in immunological screening of cDNA expression libraries.
 XX
 XX Disclosure; Page 51; 62pp; English.
 PS
 XX Polynucleotide sequences AAC79348-C79375 encode plant viral movement
 CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
 CC to establish systemic infections via movement proteins that utilize
 CC existing plant pathways to traffic macromolecules to surrounding cells.
 CC proteins such as those of the invention are similar to viral movement
 CC proteins that function in the transport of nucleic acids from cell to
 CC cell. The plant viral movement proteins are useful for obtaining a
 CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
 CC encoding the plant viral movement proteins are useful for positive
 CC selection of a transformed cell. The proteins are useful in the field of
 CC plant molecular biology, and in the preparation of antibodies against the
 CC proteins. The proteins are also useful for isolating cDNAs and genes
 CC encoding homologous proteins from the same or other plant species, and to
 CC create transgenic plants in which the protein is presented at higher or
 CC lower levels than normal or in cell types or developmental stages in
 CC which they are not normally found. The proteins and nucleotide sequences
 CC may be used to control cosuppression and engineer plant virus resistance
 XX
 SQ Sequence 617 BP; 147 A; 160 C; 176 G; 133 T; 0 U; 1 Other;
 Query Match 25.0%; Score 219; DB 3; Length 617;
 Best Local Similarity 75.1%; Pred. No. 5.2e-57;
 Matches 299; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
 QY 52 GCGAGGACGCGAGGAGGACATGTCACGCGGACGCTGGAAGTGTCTGCTGGGCGCAA 111
 Db 208 GCCAACCCGCGGAGGAGAGATGGCGCGGAGCGCTGGAGGTGCTTCTGTCGAGCCAG 267
 QY 112 GGGCTCTCAGAACACCGATTACTCTGTAACATGATCCGTATGCAATTTCTCAAGTCCG 171
 Db 268 GGGCTCTCAGAACACCGATTACTCTGAGCAACATGACCCCTACGGCTTCTGCAATGTCG 327
 QY 172 TTCACAGGACGAGAGACGATTTTGCAACTGGAAGAAAGAACTACCCCTGAGTGAATGA 231
 Db 328 CTCACGACGAGCAGAGAGCAGCGTCCATCTGGCAAGGCTGTGAACCTGAGTGAACGA 387
 QY 232 AAATTTTATCTTCACTGTCTGACCGGACACACACTGGTAATCAAGCTTATGACAG 291
 Db 388 GACCTTCGTTTCACTGCTCCACCGCTCCACCGCGCACANGAGCTGTTTCATCAAGCTCTCGACAG 447
 QY 292 TGATACAGGACAGCAGATGACTTTTGTGGTGAAGCAACGATTCCATTTGGAAG-CAGTGT 350
 Db 448 TGACGGTGGCACTGATGACGATTTTGTGGTGAAGCAACGATTCTCTGGAAGCCAGTTT 507
 QY 351 ATACTGAAAGGA--GCATTTCCACCAACACTCTATATGTTGTGAAGGTGAAATACTG 408
 Db 508 ACACGGAAGGAAGCATTCCTTCCGACTGTTTACAAATGTTGTGAAGACGAAAGATACCG 567
 QY 409 CGGGAAATCAAAAGTTGTTCTCAGATTCACTCTCTGAGG 446
 Db 568 CGGAGAAATCAAAAGTTGGCTCACGTTTCACTCCAGAGG 605

RESULT 12
 ADJ43944/c
 ID ADJ43944 standard; cDNA; 780 BP.
 AC ADJ43944;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Plant cDNA #4944.
 XX
 KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;

KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.

OS Eukaryota.

PN US2004016025-A1.

XX 22-JAN-2004.

PD 26-SEP-2002; 2002US-00260238.

PF 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

XX (BUDW/) BUDWORTH P.

PA (MOU/) MOUGHAWER T.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (PROV/) PROVANT N.

PA (RICK/) RIQUE D.

PA (ZHUT/) ZHU T.

PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

PI Golf SA, Katagiri F, Kreps J, Provant N, Rique D, Zhu T;

XX WPI.; 2004-190374/18.

DR New rice promoter, useful for manipulating crop plants to alter or

XX improve phenotypic characteristics, e.g. produce large quantities of oil

PT or proteins, resistance to insecticides, virus or fungi, stress tolerance

PT or high nutritional value.

XX Example 13; SEQ ID NO 4944; 230pp; English.

CC The invention relates to plant nucleotide sequences that direct seed-,

CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

CC or constitutive transcription of an operatively linked nucleic acid

CC segment. The invention also relates to a method for augmenting a plant

CC genome and a method of identifying a gene, where its expression is

CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,

CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

CC sorghum, rice or wheat. The polynucleotides and the polypeptides they

CC encode are useful for manipulating crop plants to alter or improve

CC phenotypic characteristics, to produce large quantities of oil or

CC proteins, to incur resistance to insecticides, viruses or fungi, and to

CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

CC have a high nutritional value with reduced apical dominance or dwarfism,

CC early flowering or altered metabolic pathways. This sequence represents a

CC plant nucleic acid of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification but was obtained in

CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 780 BP; 218 A; 205 C; 146 G; 211 T; 0 U; 0 Other;

Query Match

Beat Local Similarity 23.8%; Score 208.8; DB 12; Length 780;

Matches 304; Conservative 0; Mismatches 137; Indels 3; Gaps 1;

Qy 71 ATGGTCACGGGACGCTGGAGTCTGCTCTGGGGCCCAAGGCGCTCGAGAACACCGCAT 130

Db 757 ATGGTTCGTGGAACGCTGGAGGTCTCTCTGTGAGCGCCCAAGGCGCTCGAGACGTGAT 698

Qy 131 TACCTCTGTAAATCATGATTCGGTATGCAATTCCTCAAGTCCGCTTCACAGGAGCAGAGC 190

Db 697 TTCTTCGCAAAATGGATCCTTATGCGGCTCTTACGTACCGCAGTCAGGAACAGAAAGC 638

Qy 191 AGTATTGCAACTGGAAGAACTACCCCTGAGTGAATGAAAACTTTTATCTTCACTGTG 250
Db 637 AGTACTGCATCAGGTGCAGGTAGTAATCTCTGAATGGAATGAGACCTTTGTCTTTAATGTG 578
Qy 251 TCTGACCGGACAACAGACTTGGTAAATCAAGCTTATGGACAGTATACAGGACAGCAGAT 310
Db 577 TCTGACCAATGTCTCGGAGCTCATTTGTTAAATCATGGACAGTACTACTTTTCAAAAGAT 518
Qy 311 GACTTTGTGTGGAAGCAACGATTCTTCAATTTGGAAGCAGTGTATATCTGAAAGGAGCATTTCCA 370
Db 517 GATTTCTGAGGAGAACAAAATCCCATTTGAACAGTGTTCGTGGAGGAAGCCTTCAG 458
Qy 371 CCAACACTCTATATATTTGTGAAAGGTGAAAAATCTCGCGGGGAAATCAAAAGTTGGTCTC 430
Db 457 CCAACCATATACAGTGTGGTCAAGGATCAGGATACTGTGGAGAAATAAAGATCGGTCTC 398
Qy 431 ACATTCTCTCTGAGGATATCTCGCCACGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAG 490
Db 397 ACTTTCACGCCAGTGGAACTCG---AGGCTTTGACGAGGAAGCATTCGGAGGATGGAAA 341
Qy 491 CAATCATCTTAGAGCTAGATGCTT 514
Db 340 CATTCGGCATTAGGAAATGCAT 317

RESULT 13

AAC79361

ID AAC79361 standard; cDNA; 770 BP.

XX AAC79361;

AC AAC79361;

DT 06-FEB-2001 (first entry)

XX Plant viral movement protein encoding cDNA SEQ ID 27.

DE Plant viral movement protein; transport; transgenic plant;

KW viral resistance; cosuppression; ss.

XX Oryza sativa.

OS WO2000060088-A2.

PN 12-OCT-2000.

PD 06-APR-2000; 2000WO-US0009110.

PP 07-APR-1999; 99US-0128092P.

PR (DUPO) DU PONT DE NEMOURS & CO E I.

PA Krebbers E, Weng Z, Cahoon RE;

XX WPI; 2000-638467/61.

XX P-PSDB; AAB44507.

XX Novel viral movement polypeptides and polynucleotides useful in field of

PT plant molecular biology, for producing transgenic plants, to prepare

PT antibodies and in immunological screening of cDNA expression libraries.

XX Claim 2; Page 48-49; 62pp; English.

XX Polynucleotide sequences AAC79348-C79375 encode plant viral movement

CC proteins AAB44494-B44520. Some plant viruses have been shown to be able

CC to establish systemic infections via movement proteins that utilize

CC existing plant pathways to traffic macromolecules to surrounding cells.

CC Proteins such as those of the invention are similar to viral movement

CC proteins that function in the transport of nucleic acids from cell to

CC cell. The plant viral movement proteins are useful for obtaining a

CC nucleic acid fragment encoding a viral movement protein. Polynucleotides

CC encoding the plant viral movement proteins are useful for positive

CC selection of a transformed cell. The proteins are useful in the field of

CC plant molecular biology, and in the preparation of antibodies against the

Qy 471 AGGACTTCGGTGGATGAAGCAATCATCTTA 501
||||| | | | | | | | | | | | | | | |
Db 183 AGGAGTCTATGGGGCTGGAAAACTCTGA 153

RESULT 15
AAC36982
ID AAC36982 standard; DNA; 697 BP.
XX AAC36982;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15760.
XX
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-01233180P.
PR 09-MAR-1999; 99US-01233548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127452P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
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PR 07-MAY-1999; 99US-0132486P.
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PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135112P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 10-JUN-1999; 99US-0138540P.
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PR 18-JUN-1999; 99US-0139454P.
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Mon Jan 10 09:09:10 2005

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PR	18-AUG-1999;	99US-0149426P.
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PR	28-OCT-1999;	99US-0161920P.
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PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match 21.7%; Score 190.2; DB 3; Length 697;
Best Local Similarity 63.9%; Pred. No. 4.9e-48;
Matches 288; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

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Db	79	AGAGAAAACCAAAAATGCTCATGGAATCTTGAAGTTGTTCTTGTACAGGCCA	138
QY	111	AGGGCTCGAGAACACCGATTACCTCTGTATCATGGATCCGATGCAATCTCAAGTCC	170
Db	139	AAGGTCTCGAGACGAGATTTTCTGAAATACATGGATCCTTATGTGCAACTCACTTGT	198

QY	171	GTTTCACAGGACGAGAGCAGTATTGCAACTGSAAGAACTTACCCCTGAGTGAATG	230
Db	199	GGACTCAAGATCAGAAGAGCAACGTTGCAAGGAATGGGACAACTCCGGAATGGATG	258
QY	231	AAAACTTTATCTTCACTGTGTCTGACCGGACAAACAGACTTTGGTAATCAAGCTTATGACA	290
Db	259	AGACATTTATCTTCACTGTGTCTGAGGAACTACAGAGTTAAAGCGAAAATCTTCGACA	318
QY	291	GTGATACAGGACAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTCGAGCAGTGT	350
Db	319	AAGATGTCGGTACAGAGGATGATCGGTTGGTGAAGCAACTATTTCCTGAGCCGGTTT	378
QY	351	ATACTGAAAGGAGCATTCACCAACACTCTATAATGTTGTAAGGTGAAAAATACTGCG	410
Db	379	TCGTGGAAGGAAGTATTCACCAACTGCATACAAATGTTGAAGATGAAGATACAAAG	438
QY	411	GGGAAATCAAAAGTTGGTCTCATTCATTCATCTCTGAGGATACTTCGCCAGCGGGTCTCCAG	470
Db	439	GAGAGATTTGGGTGGCTCTCTCTTCAAGCCCTCGGGAACCGAAGCAGCGGGTATGGACG	498
QY	471	AGGACTTCGGTGGATGGAGCAATCATCTTA	501
Db	499	AGGAGTCCTATGGGGGCTGGAATAACTCTGA	529

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Job time : 528 secs

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OM nucleic - nucleic search, using sw model

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6226.511 Million cell updates/sec

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Perfect score: 8%

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.6	5.1	7218	1	US-08-232-463-14, Appl
2	37.2	4.2	1141	4	US-09-806-708B-22
3	37.2	4.2	2958	4	US-09-688-078-5
C 4	37	4.2	2465	4	US-09-205-258-206
5	36	4.1	2229	4	US-09-799-451-554
6	36	4.1	5917	4	US-09-780-175-17
C 7	35.4	4.0	1141	4	US-09-806-708B-22
8	35.2	4.0	801	4	US-09-252-991A-4545
C 9	35.2	4.0	969	4	US-09-252-991A-4308
10	35.2	4.0	1284	4	US-09-286-981B-24
C 11	34.2	3.9	507	4	US-09-513-999C-10484
12	34.2	3.9	1548	4	US-09-248-796A-6167
C 13	33.8	3.9	710	3	US-09-988-416-256
14	33.8	3.9	11050	4	US-10-204-708-86
C 15	33.8	3.9	392000	4	US-10-027-983-11
C 16	33.6	3.8	575	4	US-09-513-999C-10483
C 17	33.6	3.8	818	4	US-09-513-999C-10485
18	33.6	3.8	1338	4	US-09-286-981B-23
19	33.6	3.8	1338	4	US-09-286-981B-26
20	33.6	3.8	1360	3	US-09-961-083-37
21	33.6	3.8	1360	4	US-09-536-784-37
22	33.6	3.8	4149	2	US-08-737-715-1
23	33.6	3.8	4723	4	US-09-023-655-1137
24	33.6	3.8	12665	4	US-08-961-527-134
C 25	33	3.8	580073	4	US-08-545-528D-1
26	32.8	3.7	837	4	US-09-270-767-3634
27	32.8	3.7	837	4	US-09-270-767-18916

28	32.8	3.7	1245	4	US-09-774-528-372	Sequence 372, Appl
29	32.6	3.7	319608	4	US-09-539-333D-1	Sequence 1, Appli
30	32.6	3.7	250	1	US-08-480-552-16	Sequence 16, Appl
31	32.6	3.7	250	3	US-08-929-208-16	Sequence 16, Appl
32	32.6	3.7	250	3	US-09-568-315-16	Sequence 16, Appl
33	32.6	3.7	366	4	US-09-513-999C-8827	Sequence 8827, Ap
C 34	32.6	3.7	399	4	US-09-621-976-8976	Sequence 8976, Ap
35	32.6	3.7	90541	4	US-09-759-359A-3	Sequence 3, Appli
36	32.6	3.7	90541	4	US-10-207-973-3	Sequence 3, Appli
37	32.6	3.7	1664976	4	US-08-916-421B-1	Sequence 1, Appli
38	32.6	3.7	1664976	4	US-09-692-570-1	Sequence 1, Appli
39	32.4	3.7	1148	4	US-09-665-189A-75	Sequence 75, Appl
40	32.4	3.7	1908	4	US-09-543-681A-3327	Sequence 3327, Ap
41	32.4	3.7	2855	4	US-09-904-420A-1	Sequence 16, Appl
42	32.4	3.7	3831	4	US-09-215-450-16	Sequence 16, Appl
43	32.4	3.7	53332	4	US-09-801-861-3	Sequence 3, Appli
44	32.4	3.7	53332	4	US-10-224-562-3	Sequence 3, Appli
45	32.4	3.7	319608	4	US-09-679-409-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/232,463
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-Fis
; US-08-232-463-14

Query Match

5.1%; Score 44.6; DB 1; Length 7218;

Best Local Similarity 2.2%; Pred. No. 0.00082;
Matches 8; Conservative 207; Mismatches 146; Indels 0; Gaps 0;

QY 3 ACCAGCTTCGTTACGCCACAGCAAGGCACAGGGCTTGTGAGGAGAGCGAGCGG 62
Db 1447 AAGAAATTGGTACRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 1388

QY 63 AGAGGACATGGTGCACGGGACCTGGAAGTGTCTGCTGGGGCGCAAGGGCTCGAGA 122
Db 1387 RRR 1328

QY 123 ACACGATTAACCTCTGTAACATGATCGGTATGCAATCTCAAGTCCGCTTCACAGGAC 182
Db 1327 RRR 1268

QY 183 AGAAGACAGTATTGCACTGGAAGAAAGAACTACCCCTGAGTGAATGAAACTTTATCT 242
Db 1267 RRR 1208

QY 243 TCACTGTGTCTGACCGGACAAAGAGCTTGGTAATCAAGCTTATGGACAGTGATACAGGCA 302
Db 1207 RRR 1148

QY 303 CAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGA 362
Db 1147 RRR 1088

QY 363 G 363
Db 1087 R 1087

RESULT 2
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 4.2%; Score 37.2; DB 4; Length 1141;
Best Local Similarity 8.7%; Pred. No. 0.072;
Matches 47; Conservative 235; Mismatches 259; Indels 2; Gaps 1;

QY 211 AACTACCCCTGAGTGAATGAAACTTTATCTTCACTGTGTCTGACCGGACACAGACTT 270
Db 62 ARMYKYRRYNNKSRWGWYKKWYBCANNITSBRYHARRWKDMKTAYBMTWTKWGKT 121

QY 271 GGTAATCAAGCTTATGACAGATGATACAGCAGCAGATGACTTTGTTGGTGAAGCAAC 330
Db 122 GWRHRYWRWRMBDVTVDHHYVVTAMNNAWTTTMCMDKDDKRTWRWWWKNNNAITGWD DDTKY 181

QY 331 GATTTCATTGGAAGCAGTGTATCTGAAAGGACATTTCCACCAACACTCTATAATGTTCT 390
Db 182 HMNNNGCBTVTWVYKTRDWSBRMNYGMBWKNWSYDVYTVVWVDDMKCKVRKW 241

QY 391 GAAAGGTG--AAAAATACTGCGGGGAAATCAAAGTTGGTCTCACATTCACCTCCTGAGGAT 448

Db 242 VTRGRMRNMYMVBTAHRRYYNNGWTBAMAYRRRTWNNNNNNNAKAMCKRAKYWGNRAB 301

QY 449 ACTCCCGCAGCGGGTCTCCAGAGACTTCGGTGTGATGGAAGCAATCATCTTAGAGCTAG 508
Db 302 VNSTCTTWAASKTTKVRTSCWANNCRAGDANKDHKWKWMSAAMGVVYNNNNNNNNWYTKKAR 361

QY 509 ATGCTTTAAGGGTGCACGAGAGCAGAGCAAAATTCATGCGCTTGGAGCCTTCAGCGCTC 568
Db 362 HBARNDWVWHSKWKHANAAHYSRKKWTBYKRTWVNNNGTTWVKRWAWYWKMDMDW 421

QY 569 GAGTACTTCACTGAATGCAAAATTCATTCGATTTGGCTCTTTTGAATGTTTTCAGAGA 628
Db 422 BGTNNNNNGRTYGYGWTGNKQWTVYKWKANNCKWRAWDHKTCTHNNNTTMMKMTYWN 481

QY 629 AGTGTTATTAGTAGCTTTCAACAAAAATAGTCCATATTCCTCTATATCCCGTATTGA 688
Db 482 CYWKSMTNGKSHRBAAAVYTWYMWRRYAHANNNNNDYMWKACTWYKYBVCSKWNYYA 541

QY 689 AATTCTAAGCGCGTTTGTGATTACTGCTTACAAACAAGAGTTTGTCTCTAGTTCCTCACT 748
Db 542 AWYTKSSWNYTSRYRWKNNNSWRWSRSDTRSGRANNYARABHYGYKWNTRWBWSHTWB 601

QY 749 ACQ 751
Db 602 HBR 604

RESULT 3
US-09-688-078-5
; Sequence 5, Application US/09688078
; Patent No. 6660483
; GENERAL INFORMATION:
; APPLICANT: Kask, Kalev
; APPLICANT: Melcher, Thorsten
; APPLICANT: Chin, Daniel J.
; TITLE OF INVENTION: DIAGNOSTIC MARKER FOR NEUROLOGICAL CONDITIONS
; FILE REFERENCE: 019488-001310US
; CURRENT APPLICATION NUMBER: US/09/688,078
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/159,622
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2958
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-688-078-5

Query Match 4.2%; Score 37.2; DB 4; Length 2958;
Best Local Similarity 50.6%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 90; Conservative 0; Indels 88;

QY 179 GAGCAGAGAGCAGATGTTGCAACTGCAAAAGAACTACCCCTGAGTGAATGAAAACTTT 238
Db 2105 GAACAGAGAGCAGAAAACCTGTGAACAGATGGAGATGCTCTATGTTGATGAAGCTTT 2164

QY 239 ATCTTCACTGTCTGACCGGACAAACAGACTTGGTAATCAAGCTTATGGACAGTGTACA 298
Db 2165 GAAATTTCAAAATCAACCTCCCGAACTAGCCATGGTGGCGCTTTGTAGTGTGGATGATGAC 2224

QY 299 GGCACAGCAGAGTCTTTGTTGGTGAAGCAACGATTTCCATTGGAAGCAGTGTATCTG 356
Db 2225 TACATTGGCGATGAATTTATTGGCCAGTACACGATTCCTCTTGAATGTTTACAAACGG 2282

RESULT 4
US-09-205-258-206/c
; Sequence 206, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 206
; LENGTH: 2465
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-205-258-206

Query Match 4.2%; Score 37; DB 4; Length 2465;
Best Local Similarity 50.9%; Pred. No. 0.14;
Matches 88; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 370 ACCAACACTCTATAATGTTGTGAAAGGTGAAATACTGCGGGGAAATCAAAGTTGGTCT 429
Db 2400 AGCAAAAGTAGTTTGTGTTCAATCTTAACATATAATACATTTTAAGTCATTATGAAAT 2341

Qy 430 CACATTCACCTCTGAGGATACCTGCCNAGCGGGGTCTCCAGAGGACCTTCGGTGGATGAA 489
Db 2340 TTCATTTTTTGTGTATTTTCACTGTAGTGTGTGACAAACAAATGACATCTGTGTACCAGA 2281

Qy 490 GCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCACCAGAGCAGCAGGACAAT 542
Db 2280 GCATACATATATCAACAGTAGATGTAATTTTTCATTACATCACTGCTAGTAAAT 2228

RESULT 5
US-09-799-451-554
; Sequence 554, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yuning
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 554
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (150)..(1694)

US-09-799-451-554

Query Match 4.1%; Score 36; DB 4; Length 2229;
Best Local Similarity 47.7%; Pred. No. 0.29;
Matches 105; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 102 TTGGGCGCAGGCGCTCGAGAACCCGATTACCTCTGTAAACATGATCGGTATGCAATTC 161
DB 247 TTGAAGGGAGAGACCTCAAGGCCATGGATTCACAGGGTTGAGCGATCCCTACGTGAAGT 306

QY 162 TCAAGTGCCTGTTCCACAGGAGCAGACGAGTATTCGAACTGGAAGAACTACCCCTG 221
DB 307 TCCGGCTTGGCATCAGAAGTACAAGCAAGATTATGCAAAAGCTTGAATCCTCAGT 366

QY 222 AGTGGAAATGAAACTTTATCTTCACTGTGTGACCGGACACAGACTTGGTAATCAAGC 281
DB 367 GGAGGGAACAATTTGATTTTCACTTTATGAAGAAAGAGGAGTGCATTTGATATCACTG 426

QY 282 TTATGACAGTGTATACAGGCACAGCAGATGACTTTTCTG 321
DB 427 CATGGGACAAAGATGCTGGGAAAGGATGATTTTCATTTG 466

RESULT 6

US-09-780-175-17
Sequence 17, Application US/09780175
Patent No. 6440738

GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RTS-0184
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 17
LENGTH: 5917
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1634)...(1990)
NAME/KEY: CDS
LOCATION: (2876)...(2750)
NAME/KEY: CDS
LOCATION: (3344)...(3382)
NAME/KEY: CDS
LOCATION: (3969)...(3992)
NAME/KEY: CDS
LOCATION: (4185)...(4403)
NAME/KEY: CDS
LOCATION: (4670)...(4735)
US-09-780-175-17

Query Match 4.1%; Score 36; DB 4; Length 5917;
Best Local Similarity 62.0%; Pred. No. 0.57; Indels 35; Gaps 0;
Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 34 AGGGGCTTGTGAGGAGAGCGAGGAGCGGAGGAGGACATGGTCACGGGACGCTGGAAGT 93
DB 3102 AGGGAGTTGGAGGAGAGCAAGAGGAGCAGAGGCTGAAAGGCTGTGAGGGGAGGAGCAGC 3161

QY 94 GCTGCTCTGGGGCCAAAGGCTTCGGAACA 125
DB 3162 TGTCTCTGTTGATGCAAGGCTCAGAAAGCCCA 3193

RESULT 7

US-09-806-708B-22/c
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:

APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)...(1141)
OTHER INFORMATION: Consensus sequence of A.t., L.a., and B.n. FABL promoters
US-09-806-708B-22

Query Match 4.0%; Score 35.4; DB 4; Length 1141;
Best Local Similarity 8.6%; Pred. No. 0.29; Indels 0; Gaps 0;
Matches 48; Conservative 224; Mismatches 283; Indels 0; Gaps 0;

QY 70 CATGTCACGGGAGCGTCTGCTCTGCTGGGCGCAAGGCGCTCGAGAACACCGA 129
DB 681 VMRRRMTNTKTRWYSTTTRHHYTGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 622

QY 130 TTACCTCTGTAACATGATCGTATGCAATTCCTCAAGTCGCGTTCACAGGAGCAGAAG 189
DB 621 DGMTVRKKVKWRDITCTTYVDVWADSWWVWYANMMRCRDVTYTRNNYCKSAHVSWSN 562

QY 190 CAGTATTGCAACTGAGAAAGGAACCTACCCCTGAGTGAATGAAAACTTTATCTTCACTGT 249
DB 561 NAMVRRYSARNSSMARWTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 502

QY 250 GTTCACCGGACACAGACTTGGTAATCAAGCTTATGACAGTATGACGACAGCAGCAGA 309
DB 501 ARBTTTVYDSCNAKSMWRGNMWRAMKMWAAANNNDAGAMDHWTYWMGNNTMMRRAWK 442

QY 310 TGACTTTGTTGGTGAAGCAACGATTCCTTGAAGCAGTGTATATCTGAAAGGAGCATTC 369
DB 441 NMACRRAYCCNN 382

QY 370 ACCAACACTCTATAATGTTGTAAGAGTGAAAAATACTCGCGGGAATAACAAAGTTGGTCT 429
DB 381 TNTDMMWTSDBWHYIVDYTMRAWNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 322

QY 430 CACATTCCTCTGAGGATATCTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGA 489
DB 321 WGSAYBMAAMSMAAGASNBVTYNWCWRTYMGKTMNTNNNNNNNNNNNNNNNNNNNN 262

QY 490 GCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCCAGCAGACAGCAGCAATTCATGG 549
DB 261 YYDTAVWTBKRNKYCYAYBYMYMGKHWHWRRABHRSNNNNNNNNNNNNNNNNNNNN 202

QY 550 CTTGGAGCCTTCAGCGCTCGAGTACTTCATGTAATGAGAAATTCATTCGATTTGGCTTC 609
DB 201 HAMRVBKWABAVGCNNNNKDRMAHHWCATNNNNNNNNNNNNNNNNNNNNNNNNNN 142

QY 610 TTTTCATTTTCAG 624
DB 141 RDDBAHVKTYWYR 127

RESULT 8

US-09-252-991A-4545
Sequence 4545, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

```
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4545
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4545

Query Match          4.0%; Score 35.2; DB 4; Length 801;
Best Local Similarity 53.7%; Pred. No. 0.27;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 56 GGACGGAGGAGGACATGCTGCACGGACGCTGGAAGTGTCTGCTGGGGCCCAAGGC 115
Db 109 GGGCGGAAGTGGAGATCGGTGAAGGACGGTGATCGGTCGCGACGTGGTCTCAAGGC 168

Qy 116 CTCGAGAACACCGATTACCTCTGTAACATGGATCCGTATGCAATTCCTCAAGTCCGTTCA 175
Db 169 CCCACGAAGATCGGACAGCACACCGCATCTACCAGTTTCCACGGTCGGCGAGGATACT 228

Qy 176 CAGGACGAGAGAGCA 191
Db 229 CCCGACCTGAATACA 244

RESULT 9
US-09-252-991A-4308/c
; Sequence 4308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4308
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4308

Query Match          4.0%; Score 35.2; DB 4; Length 969;
Best Local Similarity 53.7%; Pred. No. 0.3;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 56 GGACGGAGGAGGACATGCTGCACGGACGCTGGAAGTGTCTGCTGGGGCCCAAGGC 115
Db 708 GGGCGGAAGTGGAGATCGGTGAAGGACGGTGATCGGTCGCGACGTGGTCTCAAGGC 649

Qy 116 CTCGAGAACACCGATTACCTCTGTAACATGGATCCGTATGCAATTCCTCAAGTCCGTTCA 175
Db 648 CCCACGAAGATCGGACAGCACACCGCATCTACCAGTTTCCACGGTCGGCGAGGATACT 589

Qy 176 CAGGACGAGAGAGCA 191
Db 588 CCCGACCTGAATACA 573

RESULT 10
US-09-286-981B-24
; Sequence 24, Application US/09286981B
; Patent No. 6503511
```

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; GENERAL INFORMATION:
; APPLICANT: Wizemann, Theresa M.
; APPLICANT: Koenig, Scott
; APPLICANT: Johnson, Leslie S
; TITLE OF INVENTION: Derivatives of Choline Binding Proteins for Vaccines
; FILE REFERENCE: 469201-396
; CURRENT APPLICATION NUMBER: US/09/286,981B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: US 60/085,743
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA derived
; OTHER INFORMATION: from the genome of Streptococcus pneumoniae
; US-09-286-981B-24

Query Match          4.0%; Score 35.2; DB 4; Length 1284;
Best Local Similarity 53.7%; Pred. No. 0.37;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 287 GACAGTGATACAGGCACAGCAGATGACTTTTGTGGTGAAGCAACGATTCATTGGAAAGCA 346
Db 733 GAAATGATCGGAAGTCTTCAGATTCTAGCGTAGGTGAAGAACTCTTCCAGGCCCATCC 792

Qy 347 GTCTATACTGAAAGGAGCATTCCACCACACTCTATATGTGTGAAAGGTGAAAAATAC 406
Db 793 CTGAAACCAAGAAAAAGGTTGCAGAAGCTGAGAAGAGGTTGAAGAAGCTTAAGAAAAA 852

Qy 407 TCGCGGGGAATCAAG 422
Db 853 GCCGAGGATCAAAAAG 868
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RESULT 11

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US-09-513-999C-10484/c
; Sequence 10484, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10484
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 36
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 266
; OTHER INFORMATION: n=a, g, c or t
; US-09-513-999C-10484
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Query Match          3.9%; Score 34.2; DB 4; Length 507;
Best Local Similarity 46.9%; Pred. No. 0.42;
Matches 105; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
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QY 539 CAATTCATCGGCTTGAGCCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGATTCATTC 598
Db 367 CTATTGAGAAGCTGCGGGCCAGCAGCAGCCAGTACAATATGCTGCAGCATTAATTGTGCA 308
QY 599 GATTTGGCTTCTTTTTCATGTTTTCAGAAGAAGTGTATTAGTGAGTTTCAACAAAAATA 658
Db 307 GGCCAACTTCACACATATTTTGGCAGTTCGTGTGCATACNTGGCAGACTATCATATC 248
QY 659 GTCCCATATGCTCTATATCCCGTATTGGAATTCCTAAGCCGCTTTGTGATTAAGTCTTA 718
Db 247 CCCCTCTACGGGCATAAGCAATCTGACAAATGATATCTCTGTTTGTACACGAACATAT 188
QY 719 CAACAGAAGTTTGTCTTCTAGTTCACATCGCTTTTGTGA 762
Db 187 CATCCTGTATTGGGTGTGTGTATTTATTTTATCTTGTATCA 144

RESULT 12
US-09-248-796A-6167
; Sequence 6167, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6167
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6167

Query Match 3.9%; Score 34.2; DB 4; Length 1548;
Best Local Similarity 49.2%; Pred. No. 0.91;
Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 247 TGTCTCTGACGGACACAGACTTTGGTAATCAAGCTTTATGGACAGTGATACAGGCACAGC 306
Db 381 TGTCAACAGATCAACCAAGACGAGAGAAATAGAGTTGCTGAACCTTAAGAACTCTCAGC 440
QY 307 AGATGACTTTTGGTGAAGCAACGATTCCATTGGAAAGCAGTGATATCTGAAAGGAGCAT 366
Db 441 TGCATCCGAGGTAGAAGAACAAAACTTGAAGAAAGATGCTGCTGAACCAAGAAATCAAGA 500
QY 367 TCCACCAACTCTATTAATGTTGTAAGGTGAAGAAATATCTGGGGGAAATCAAGTTGG 426
Db 501 TGGAGAAGCACTCAAGGCGATGACAAATTTGAAAAAACAATCAAGAGAAACCCCAATTGA 560
QY 427 TCT 429
Db 561 ACT 563

RESULT 13
US-08-998-416-256/c
; Sequence 256, Application US/08998416
; Patent No. 6239284
; GENERAL INFORMATION:
; APPLICANT: Philippaen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
```

```
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/S-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1225RP
; US-08-998-416-256

Query Match 3.9%; Score 33.8; DB 3; Length 710;
Best Local Similarity 49.4%; Pred. No. 0.72;
Matches 117; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 218 CCTGAGTGGAAATGAAACTTTTATCTTCACTGTGTGTCGACCGACAAACAGACT---TGGTA 274
Db 397 CCTGTTTGGACGACAGACACATCCCTGCAGTTTGAATAACCGGATTAACAACACTACCTGCGC 338
QY 275 ATCAAGCTTATGACAGTATACAGCAGCAGCAGATGACTTTTGGTGAAGCAACGATT 334
Db 337 ATCAAGGTCATGAGTGGGATGCCGGAACAGTGACGATCTCTATTGGCCACCGACCATC 278
QY 335 CCATTGGGAAGCAGTGTATCTGAAAGGAGCATTCCACCAACACTCTATAATGTTGTGAAA 394
Db 277 GCTCTAGCTGAGTGGACCCACAGTGAACCCCAATGGAAGTCCAGCTAACTGGTCTCT 218
QY 395 GGTGAAAAATATCTGGCGGGAATCAAGTTGTTCTCAATTCACTTCCTGAGGATACT 451
Db 217 AACGGCGAGGACGGTGGTATTCTTACTTGAACCTTCAAAATTTTCTCTAGGTACACT 161

RESULT 14
US-10-204-708-86
; Sequence 86, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: FIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
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; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 86
; LENGTH: 11050
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-86

Query Match          3.9%; Score 33.8; DB 4; Length 11050;
Best Local Similarity 54.4%; Pred. No. 4.9;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 608 TCTTTTGATGTTTCAGAGAAGTGTTATTAGTGAGTTTCAACAAAAATAGCTCCATAT 667
Db 171 TTTTATTATTTTGTGAAGATGTTTATAGAGAGTTGTTATATAATGAATATGTGTAT 230

Qy 668 TGCCTATATCCCGTATTGGAATCTAAGCCGTTTGTGATTACTGCTTACACACAGAA 727
Db 231 ATATATGTAAGTGTTTAGGATAGTATTCGGTACGTAGTAAATATTCGATAAATGAGTGA 290

Qy 728 GTTTT 732
Db 291 TTTT 295

RESULT 15
US-10-027-983-11/c
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217

; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (195242)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
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; LOCATION: (223581)...(224080)
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; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(2366651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
; US-10-027-983-11

Query Match          3.9%; Score 33.8; DB 4; Length 392000;
Best Local Similarity 54.4%; Pred. No. 57;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

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(without alignments)

8591.999 Million cell updates/sec

Title: US-09-913-569B-5

Perfect score: 876

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	847.4	96.7	1129	18	US-10-425-115-144798
2	846.4	96.6	1027	16	US-10-425-114-15989
3	291.6	33.3	821	17	US-10-437-963-96494
4	267	30.5	868	18	US-10-425-115-152761
5	247.2	28.2	787	16	US-10-425-114-23609
6	228	26.0	442	16	US-10-260-238-772
7	214.6	24.5	740	17	US-10-437-963-41540
8	208.8	23.8	780	16	US-10-260-238-4944
9	199.4	22.8	804	17	US-10-767-701-11176
10	193.2	22.1	782	17	US-10-437-963-87038
11	191.8	21.9	615	9	US-09-770-149-836
12	180.2	20.6	660	18	US-10-425-115-122378

13	174.8	20.0	718	16	US-10-425-114-22597	Sequence 22597, A
14	174.8	20.0	741	16	US-10-425-114-2939	Sequence 2939, Ap
15	173.6	19.8	1294	18	US-10-425-115-106431	Sequence 106431, A
16	172	19.6	866	18	US-10-425-115-11791	Sequence 11791, A
17	171.8	19.5	856	18	US-10-425-115-11787	Sequence 11787, A
18	170.4	19.5	762	16	US-10-425-114-27551	Sequence 27551, A
19	168.2	19.2	429	16	US-10-260-238-5911	Sequence 5911, Ap
20	168	19.2	1196	18	US-10-425-115-167111	Sequence 167111, A
21	162.6	18.6	646	16	US-10-425-114-11809	Sequence 11809, A
22	108.8	12.4	441	17	US-10-437-963-33381	Sequence 33381, A
23	100.2	11.4	601	18	US-10-425-115-8248	Sequence 8248, Ap
24	77.2	8.8	523	16	US-10-424-599-110802	Sequence 110802, A
25	76.2	8.7	1617	18	US-10-425-115-165068	Sequence 165068, A
26	74.6	8.5	248	16	US-10-424-599-9308	Sequence 9308, A
27	74.2	8.5	370	11	US-09-922-293-1148	Sequence 1148, Ap
28	69.6	7.9	367	16	US-10-424-599-136395	Sequence 136395, A
29	69.6	7.9	704	17	US-10-767-701-631	Sequence 631, App
30	68.8	7.9	808	16	US-10-424-599-77758	Sequence 77758, A
31	68.4	7.8	391	11	US-09-922-293-3492	Sequence 3492, Ap
32	67.6	7.7	388	16	US-10-424-599-72831	Sequence 72831, A
33	58.8	6.7	1848	18	US-10-425-115-30879	Sequence 30879, A
34	58.2	6.6	1238	18	US-10-739-930-1595	Sequence 1595, Ap
35	57.4	6.6	840	9	US-09-938-842A-2543	Sequence 2543, Ap
36	57.4	6.6	840	11	US-09-938-842A-2543	Sequence 2543, Ap
37	55	6.3	99	9	US-09-294-093B-3721	Sequence 3721, Ap
38	49.4	5.6	159	16	US-10-424-599-53762	Sequence 53762, A
39	49.2	5.6	80	9	US-09-923-876-3209	Sequence 3209, Ap
40	49.2	5.6	80	10	US-09-923-876-3209	Sequence 3209, Ap
41	49	5.6	946	16	US-10-424-599-118274	Sequence 118274, A
42	48.8	5.6	861	17	US-10-437-963-44106	Sequence 44106, A
43	48	5.5	622	17	US-10-767-795-5525	Sequence 5525, Ap
44	47.8	5.5	385	17	US-10-767-701-11177	Sequence 11177, A
45	46.8	5.3	1515	17	US-10-437-963-50658	Sequence 50658, A

ALIGNMENTS

RESULT 1
US-10-425-115-144798
; Sequence 144798, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 144798
; LENGTH: 1129
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_63541C.1
US-10-425-115-144798

Query Match	96.7%	Score	847.4	DB	18	Length	1129
Best Local Similarity	99.1%	Pred. No.	1.7e-253				
Matches	863	Conservative	0	Mismatches	6	Indels	2
Gaps	1						
Qy	8	GTTCGTTTCACGCCACAGGACGACAGGGCTTGTGAGGAGAGCGAGGAGGAG	67				
Db	221	GTTCGTTTCACGCCACAGGACGACAGGGCTTGTGAGGAGAGCGAGGAGGAG	280				
Qy	68	GACATGTTGACGGGACGCTGGAAGTCTCTCTGTTGGGCGCAAGGCCCTCGAGAACCC	127				
Db	281	GACATGTTGACGGGACGCTGGAAGTCTCTCTGTTGGGCGCAAGGCCCTCGAGAACCC	340				

```
QY 128 GATTACTCTGTAAACATGATCGTATGCAATTTCTCAAGTGCCTTACAGGAGCAGAAG 187
|
|
|
Db 341 GATTACTCTGTAAACATGATCGTATGCAATTTCTCAAGTGCCTTACAGGAGCAGAAG 400
|
|
|
QY 188 AGCAGATTGCAACTGGAAGGAAGAACTACCCCTGAGTGAATGAAACTTTATCTTCACT 247
|
|
|
Db 401 AGCAGATTGCAACTGGAAGGAAGAACTACCCCTGAGTGAATGAAACTTTATCTTCACT 460
|
|
|
QY 248 GTGCTGACCGGACAACAGACTTTGGTAAATCAAGCTTATGGACAGTGAATCAGGACAGCA 307
|
|
|
Db 461 GTGCTGACCGGACAACAGACTTTGGTAAATCAAGCTTATGGACAGTGAATCAGGACAGCA 520
|
|
|
QY 308 GATGACTTTTGTGCTGAAGCAAGCTTCCATTGGAAGCAGTGTATCTGAAGAGGACATT 367
|
|
|
Db 521 GATGACTTTTGTGCTGAAGCAAGCTTCCATTGGAAGCAGTGTATCTGAAGAGGACATT 580
|
|
|
QY 368 CCACCAACACTCTATTAATGTTGTAAGGTGAAAAATACTGCGGGGAAATCAAAAGTTGGT 427
|
|
|
Db 581 CCACCAACACTCTATTAATGTTGTAAGGTGAAAAATACTGCGGGGAAATCAAAAGTTGGT 640
|
|
|
QY 428 CTCACATTCACCTCTGAGGACTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGG 487
|
|
|
Db 641 CTCACATTCACCTCTGAGGACTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGG 700
|
|
|
QY 488 AAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCACAGAGCAGCAGCACAATTCATG 547
|
|
|
Db 701 AAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCACAGAGCAGCAGCACAATTCATG 760
|
|
|
QY 548 CGCTTGGAGCCTTCAGCCGFCGAGTACTTCATGCTAATGCAGAAATTCATTTCGATTTGGCT 607
|
|
|
Db 761 CGCTTGGAGCCTTCAGCCGFCGAGTACTTCATGCTAATGCAGAAATTCATTTCGATTTGGCT 820
|
|
|
QY 608 TCTTTTGTATTTTCAGAGAAGTGTATTAGTAGGTTCACAAAAAATAGCTCCATAT 667
|
|
|
Db 821 TCTTTTGTATTTTCAGAGAAGTGTATTAGTAGGTTCACAAAAAATAGCTCCATAT 880
|
|
|
QY 668 TGCTCTATATCCCGTATGGAAATCTTAAGGCGTTTGTGATTACTGCTTACAAACAAGAA 727
|
|
|
Db 881 TGCTCTATATCCCGTATGGAAATCTTAAGGCGTTTGTGATTACTGCTTACAAACAAGAA 940
|
|
|
QY 728 GTTTTGTCTTACTGTTCCCACTACGC--TTTTTTTTGAAAGTTTGTAGTGGAAACATCTTTGT 785
|
|
|
Db 941 GTTTTGTCTTACTGTTCCCACTACGCCTTTTGTGAAAGTTTGTAGTGGAAACATCTTTGT 1000
|
|
|
QY 786 GTTCAACGTTTGGGAGGTGTAGCCAGTAATCTCGAAGAAGGAATATTTCCCTTGC 845
|
|
|
Db 1001 GTTCAACGTTTGGGAGGTGTAGCCAGTAATCTCGAAGAAGGAATATTTCCCTTGC 1060
|
|
|
QY 846 AGCAACATTGTTTTTGTGATCCTTGAAAAA 876
|
|
|
Db 1061 AGCAATATTGTTTTTGTGATCCTTGACNA 1091
|
|
|
```

RESULT 2

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US-10-425-114-15989
; Sequence 15989, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaeka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15989
; LENGTH: 1027
; TYPE: DNA
```

```
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-020-Cl2_FLI
US-10-425-114-15989
```

```
Query Match 96.6%; Score 846.4; DB 16; Length 1027;
Best Local Similarity 99.0%; Pred. No. 3.4e-253;
Matches 863; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
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```
QY 8 GTTCTTCAACGCAACAGGCAAGGCTTGTAGGGAGAGCGAGGACGGAGGAG 67
|
|
|
Db 145 GTTCTTCAACGCAACAGGCAAGGCTTGTAGGGAGAGCGAGGACGGAGGAG 204
|
|
|
QY 68 GACATGTTGACGGGACCGCTGGAAGTGTCTCTGTTGGGCGCAAGGCTCCGAGACAC 127
|
|
|
Db 205 GACATGTTGACGGGACCGCTGGAAGTGTCTCTGTTGGGCGCAAGGCTCCGAGACAC 264
|
|
|
QY 128 GATTACCTCTGTAAACATGGATCCGTATGCAATTTCTCAAGTGCCTTACAGGAGCAGAAG 187
|
|
|
Db 265 GATTACCTCTGTAAACATGGATCCGTATGCAATTTCTCAAGTGCCTTACAGGAGCAGAAG 324
|
|
|
QY 188 AGCAGTATTGCAACTTGGAAAAAGAACTACCCCTGAGTGAATGAAAACTTTATCTTCACT 247
|
|
|
Db 325 AGCAGTATTGCAACTTGGAAAAAGAACTACCCCTGAGTGAATGAAAACTTTATCTTCACT 384
|
|
|
QY 248 GTGCTGACCGGACAACAGACTTTGCTAATCAAGCTTATGGACAGTGAATCAGGACAGCA 307
|
|
|
Db 385 GTGCTGACCGGACAACAGACTTTGCTAATCAAGCTTATGGACAGTGAATCAGGACAGCA 444
|
|
|
QY 308 GATGACTTTTGTGTAAGCAACGATTCATTGGAAGCAGTGTATCTGAAAGGAGCAATT 367
|
|
|
Db 445 GATGACTTTTGTGTAAGCAACGATTCATTGGAAGCAGTGTATCTGAAAGGAGCAATT 504
|
|
|
QY 368 CCACCAACACTCTATAATGTTGTGAAAGGTGAAAAATACTGCGGGGAAATCAAAAGTTGGT 427
|
|
|
Db 505 CCACCAACACTCTATAATGTTGTGAAAGGTGAAAAATACTGCGGGGAAATCAAAAGTTGGT 564
|
|
|
QY 428 CTCACATTCACCTCTGAGGACTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGG 487
|
|
|
Db 565 CTCACATTCACCTCTGAGGACTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGG 624
|
|
|
QY 488 AAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCACAGAGCAGCAGCAATTCATG 547
|
|
|
Db 625 AAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCACAGAGCAGCAGCAATTCATG 684
|
|
|
QY 548 CGCTTGGAGCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGAAATTCATTTCGATTTGGCT 607
|
|
|
Db 685 CGCTTGGAGCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGAAATTCATTTCGATTTGGCT 744
|
|
|
QY 608 TCTTTTGTATTTTCAGAGAAGTGTATTAGTAGGTTCACAAAAAATAGCTCCATAT 667
|
|
|
Db 745 TCTTTTGTATTTTCAGAGAAGTGTATTAGTAGGTTCACAAAAAATAGCTCCATAT 804
|
|
|
QY 668 TGCTCTATATCCCGTATTTGGAATTTCTAAGGCGTTTGTGATTACTGCTTACAAACAAGAA 727
|
|
|
Db 805 TGCTCTATATCCCGTATTTGGAATTTCTAAGGCGTTTGTGATTACTGCTTACAAACAAGAA 864
|
|
|
QY 728 GTTTTGTCTTACTGTTCCCACTACGC---TTTTTTTTGAAAGTTTGTAGTGGAAACATCTTTG 784
|
|
|
Db 865 GTTTTGTCTTACTGTTCCCACTACGCCTTTTGTGAAAGTTTGTAGTGGAAACATCTTTG 924
|
|
|
QY 785 TGTTCAAAGTTTGGGAGGTGTAGCCAGTAATCTGCAAGAAGGAATATTTCCCTTGG 844
|
|
|
Db 925 TGTTCAAAGTTTGGGAGGTGTAGCCAGTAATCTGCAAGAAGGAATATTTCCCTTGG 984
|
|
|
QY 845 CAGCAACATTTGTTTTTGTGATCCTTGAAAAA 876
|
|
|
Db 985 CAGCAATATTGTTTTTGTGATCCTTGAAAAA 1016
|
|
|
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RESULT 3

```
US-10-437-963-96494
; Sequence 96494, Application US/10437963
```

```
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 96494
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94586C.1
US-10-437-963-96494

Query Match      33.3%; Score 291.6; DB 17; Length 821;
Best Local Similarity 74.9%; Pred. No. 6.6e-80;
Matches 394; Conservative 0; Mismatches 124; Indels 8; Gaps 2;

Qy 47 GGAGAGCGAGGAGCGGAGGAGGACATGGTGCACGGGACGCTGGAGTGGCTGCTGTTGGG 106
Db 66 GGGGCGCGGGGAGCTGGGGAAGATGGTGCAGGGGACGCTCGAGGTGCTCGTCGCGA 125
Qy 107 GCCAAGGGCCCTCGAGAACACCGATTACCTCTGTAAACATGGATCGGTATGCAATTTCTCAAG 166
Db 126 GCCAAGGGCCCTCGAGAACACCGATTACCTGTGCACATGACCCGCTAGCGGTTCTCAA 185
Qy 167 TGGCGTTTACAGGAGCAGAGAGAGAGATTTGCAACTGGAAGAAAGAACTACCCCTGAGTGG 226
Db 186 TGGCGCTCGCAGGAGCAGAGAGAGAGAGCGGTTGCGTCAAGTAAAGGATCTGACCCCTGAATGG 245
Qy 227 AATCAAAATTTATCTTTCACGTGTCTGACCGGACACAGACCTTGGTAAATCAAGCTTATG 286
Db 246 AACGAAACCTTTATGTTTCAGCGTCACTCACAACCTCAGAGCTCATCATCAAGTTGATG 305
Qy 287 GACAGTGATACAGGCACAGCAGATGACTTTTGGTGAAGCAACGATTCATTGGAAGCA 346
Db 306 GACAGTGACAGTGCGACCGATGATGTTTGGTGAAGCAACGATTTCTTTGGAAGCA 365
Qy 347 GTGTATTAAGAGGAGCATTTCCACCAACTCTTATATGTTGTGAAGGTGAAAAATAC 406
Db 366 ATCTATACAGAGGAAGCATACCCCAACTGTTTATATGTTGTGAAGGAAGAAATAC 425
Qy 407 TGGCGGGAATCAAGTTGGTCTCACAATTCATCTCAGGATACCTCCAGCGGGGTCTC 466
Db 426 CGTGGAGAAATCAAAGTGGGCGCTGACGTTCACTCAGAGGATGATCGCGATCGGGGTTTA 485
Qy 467 CCAGAG---GACTTCGGTGGATGAAGCAATCATCTT-----AGAGCTAGATGCTTTAAG 518
Db 486 TCTGAGGAAGACATTTGGTGAATGAAGCAGTCATCTTTGAGGAAGAACGACATATTTGAT 545
Qy 519 GGTGCACAGCAGCAGCAGCAATTCATTCGCTTTGGAGCCTTCAGC 564
Db 546 GTGCACTGCATCGCTATGTTAAGTCTGTGCTGGAAGCCTGGAAC 591

RESULT 4
US-10-425-115-152761
; Sequence 152761, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 152761
; LENGTH: 868
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70901C.1
US-10-425-115-152761

Query Match      30.5%; Score 267; DB 18; Length 868;
Best Local Similarity 72.3%; Pred. No. 3.3e-72;
Matches 361; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

Qy 60 CCGAGGAGGACATGGTGCACGGGACGCTGGAAGTGTGCTGTTGGGGCCAAAGGGCCTCG 119
Db 234 CCGAGAGAGAATGGCGCAGGGGACGCTGGAGGTGCTGCTCGTGGAGCCCAAGGGACTCG 293
Qy 120 AGAACACCGATTACCTCTGTAAACATGATGATCCGTATGCAATTTCTCAAGTCCGTTCAAGG 179
Db 294 AGAACACCGACTACCTCTGCAACATGACCCGCTACGCGGTTCTAAAAATGCACATCGCAGG 353
Qy 180 AGCAGAGAGCAGATTATTCACACTGGAAGAAAGAAAGAAAGTATCTCTGAATGGAACGAAACCTTTG 239
Db 354 AGCAGAAAGACACCGCTGCGCTCAGGAAGAAAGAAAGTATCTCTGAATGGAACGAAACCTTTG 413
Qy 240 TCTTCACTGTGTCTGACCGGACCAACAGACTTGGTAAATCAAGCTTATGGACAGTATACAG 299
Db 414 TGTTCACCGTCTCTGAGAATGCAACCGAGCTCGTCATCAAGCTCTCGACAGTATGATG 473
Qy 300 GCACAGCAGATGACTTTTGGTGAAGCAACGATTCATTGGAAGCAGTGTATATGAAA 359
Db 474 GCACGGACGACGACAGCGTTGGTGAAGCAACGATCCCATTTGGATGGAGTGTACACTGAAG 533
Qy 360 GGAGCATTCACCAACACACTATATGTTGTGAAGTGAAGAAATACTCGGGGAATCA 419
Db 534 GAAGACTCCCAACCACTGTTTACAATGTTGTCAAGACGAAGAGTACCGTGGAGAAATCA 593
Qy 420 AAGTGTGTCTCACAATTCATCTCCTGAGGATACCTCGCAGCGGGGTCTCCACAGAG---ACT 476
Db 594 AATTCGTCTGACGTTCACTCCGAGGAGGCTCGTATGAGGATCAACCCGAGGAAACT 653
Qy 477 TCGGTGGATGGAAGCAATCATCTTTAGAGCTAGATGCTTTAAGGGTGCACCGAGCAGCAGC 536
Db 654 ACGGTGGTGGAAACCAATCATCTTGAGAAAGTAGGTGCTTTGCTGAACACTGTTGGTGGT 713
Qy 537 GACAATTCATGCGCTTGA 555
Db 714 GACAAGTCGTGTCTAGAA 732

RESULT 5
US-10-425-114-23609
; Sequence 23609, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
```

```
; SEQ ID NO 23609
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB597-068-A11_FLI
US-10-425-114-23609

Query Match      28.2%; Score 247.2; DB 16; Length 787;
Best Local Similarity 76.5%; Pred. No. 4.8e-66;
Matches 303; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 52 GCAGAGAGCGGAGGAGACATGTGACGGGAGCGCTGGAGTCTCTCGTTGGGGCCAA 111
DB 60 GCTAACCGCGGAGGAGAGATGGCGAGGGGAGCGCTGGAGGTCTCTCGTGGAGCCAG 119
QY 112 GGGCCCTCGAAGAACACCGATTACCTCTGTAAACATGGATCCGTATGCAATTTCTCAAGTGC 171
DB 120 GGGCCCTCGAAGAACACCGATTACCTGTAGCAACATGGACCCCTACGCGCTTCTGCAATGTG 179
QY 172 TTCACAGGAGCAGAGAGAGATTTGCAACTGCGAAAGAACTACCCCTGAGTGGAAATGA 231
DB 180 CTCCACGAGCAGAGAGAGAGCGTCGCATCTGGCAAAAGGCTGTGAACCTGAGTGGAAACA 239
QY 232 AAATTTATCTTCACTGTCTGACCGGCAACAGACTTGGTAATCAAGCTTATGGACAG 291
DB 240 GACCTTCTGTCTTACCGTCTCCGATGGCGCAGCAGAGCTGTTTCAATCAAGCTCTGGACAG 299
QY 292 TGATACAGGACAGCAGATGACTTTGTTGGTGAAGCAACGATTCCATTTGGAAGCAGTGA 351
DB 300 TGACGGTGGCACTGATGACGATTGTTGGTGAAGCAACGATTCTCTGGAAGCAGTGA 359
QY 352 TACTGAAGGAGCATTCACCAACACTCTATATATTTGTGAAGGTGAAATATCTGCCG 411
DB 360 CACGGAAGGAAACATCCCTCCGACTGTTTACAATGTTGTGAAGAGCAAGAAATACCGCG 419
QY 412 GGAATCAAAAGTTGCTGCATTTCACTTCACTCTGAGGA 447
DB 420 AGAAATCAAAAGTTGGCCTCAGTTTCACTTCCAGGGA 455
```

```
RESULT 6
US-10-260-238-772
; Sequence 772, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 772
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-772
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Query Match      26.0%; Score 228; DB 16; Length 442;
Best Local Similarity 78.6%; Pred. No. 3.4e-60;
Matches 330; Conservative 0; Mismatches 45; Indels 45; Gaps 3;

QY 71 ATGGTGACAGGAGCGCTGGAAAGTCTCTGTTGGGGCCCAAGGCGCTTCGAGAACACCGAT 130
DB 1 ATGGTGACAGGAGCGCTGGAGGTCTCTGTCGTGGGGCCCAAGGCGCTTCGAGAACACCGAT 60
QY 131 TACTCTGTG-----ACATGGA 147
DB 61 TACCTGTGTAGCATCAGCTTTATAATTCCTAATCCTTTAAAGCGCATTTGCTTTGAACATGGA 120
QY 148 TCCGTATGCATTTCTCAAGTGCCTTTCACAGGAGCAGAGAGAGTAGTATTGCAAC-TGGAA 206
DB 121 TCCATATGCATTTCTCAAGTGCCTTTCACAGGAGCAGAGAGAGTAGCATCAGGGCA 180
QY 207 AAGGAACTACCCCTGAGTGGAAATGAAACCTTTATCTTCACTGTGTCTGACCGGACAACAG 266
DB 181 AAGGAAGTAAACCTTGAATGGAAACGAAACCTTTGCTTCAACGCTGTCTGACAAAGCTACAG 240
QY 267 ACTTGGTAAATCAAGCTTATGACAGATGATACAGGACAGCAGATGACTTTCTTGGTGAAG 326
DB 241 AGCTGTTGATCAAGCTCTTGGACAGTGATCTGCTCAGCCGAGACTTTTGTGTGTAAG 300
QY 327 CAACGATTCCATTTGGAAGCAGTGTATCTGAAAGAGAGCATTTCCACCAACACTCTATAATG 386
DB 301 CAAC-ATTCTTTTGAAGCAGTGTATCTGAAAGGAGTATTTCCACCAACTCTGTATAATG 359
QY 387 TTGTGAAAGGTGAAATACTGCGGGGAAATCAAAAGTTGGTCTCACTTCACTCTCTGAGG 446
DB 360 TTGTGAAGGATGAACATTACTGTGGAGAAATCAAAAGTCGGCTCACAATTCACCTCTGAGG 419
```

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RESULT 7
US-10-437-963-41540/c
; Sequence 41540, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41540
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44875C.1
US-10-437-963-41540
```

```
Query Match      24.5%; Score 214.6; DB 17; Length 740;
Best Local Similarity 78.8%; Pred. No. 7.1e-56;
Matches 256; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 189 GCAGTATTGCAACTGAAAGGAACTACCCCTGAGTGGAAATGAAATTTATCTTCTCAGCTG 248
DB 598 GCTATGTGATTGTGGCAAAAGGAAGTAAACCTGAATGGAAACGAAATCTTTGTTCTCCCG 539
QY 249 TGTCTGACCGGACAAACAGACTTTGGTAATCAAGCTTATGGACAGTGTATGACGACAGCAG 308
DB 538 TGTCTGACAAAGCTACAGAGCTGTTGATCAAGCTCTTGGCCAGTGTACTATGGCTCACCCG 479
```

Qy 309 ATGACTTTTGGTGAACCAAGATTCCATTGGGAAGCAGTGTATATCTGAAAGGAGCAATTC 368
Db 478 ACGACTTTTGGTGAAGCAACGATTCTCTTTGGAAACCAAGTGTATATCTGAAAGGAGTATTC 419
Qy 369 CACCAACACTCTATAATCTGTGAAAGGTGAAATACTCGCGGGAATCAAAAGTTGTC 428
Db 418 CCCACCTCTGTATATGTTGTGAAGATGACCATTCCTGTGGAGAAATCAAAAGTCGGCC 359
Qy 429 TCACATTCACCTCTGAGGATATCTCGCCAGCGGGTCTCCAGAGGACTTTCGGTGGATGGA 488
Db 358 TCCCATTCCTCTGAGGATGTTCGCCAGCGTGTCTTCCTGAGGACTTTTGGTGGATGGA 299
Qy 489 AGCAATCATCTAGAGCTAGATGCT 513
Db 298 AGCAATCTCGTTAAAAAAGCAGAT 274

RESULT 8

US-10-260-238-4944/c
; Sequence 4944, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickle, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 4944
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Musa acuminata
; US-10-260-238-4944

Query Match 23.8%; Score 208.8; DB 16; Length 780;
Best Local Similarity 68.5%; Pred. No. 4.8e-54;
Matches 304; Conservative 0; Mismatches 137; Indels 3; Gaps 1;
Qy 71 ATGGTGACCGGACGCTGGAAGTCTGCTCGTTGGGSCCAAGGCCCTCGAGAACCCGAT 130.
Db 757 ATGGTTCGTGAAACGCTGGAGTCTGCTCGTGAGCGCAAGGCGCTCGAGGACGTGAT 698
Qy 131 TACCTCTGTAACATGGATCCGTATGCAATTCCTCAAGTGCCGTTCCAGAGGACAGAGC 190
Db 697 TTCTTCGGCAAAATGGATTCCTTATGCGCTCCTTACGTACCGCAGTCAGGAACAGAAAAGC 638
Qy 191 AGTATTGCACTGGAAGGAACTACCCCTGAGTGGAAATGAAACTTTATCTTCACATGTG 250
Db 637 AGTACTGCATCAGTGCAGGTAGTAACTCTGGAATGGAATGAGACCTTTGCTTTAATGTG 578
Qy 251 TCTGACCGGACAAACAGACTTGGTAAATCAAGCTTATGGACAGTGTATACAGGCACAGCAGAT 310
Db 577 TCTGACAAATGCTCGGAGCTCATTTGTTAAATCATGACAGTGATACTTTTTCAAAAGAT 518
Qy 311 GACTTTGTTGGTGAAGCAACGATTCCATTGGAAGCAGTGTATATCTGAAAGGAGCAATTC 370
Db 517 GATTTCTGAGGAGAGCAAAATCCCATTTGGAAGCAGTGTTCGTGGGAAGGAAAGCCTCAGC 458

Qy 371 CCRAACTCTATATGTTGTGAAAGGTGAAAAATCTCGCGGGAATCAAAAGTTGGTCTC 430
Db 457 CCAACCATATACAGTGTGGTCAAGGATCAGCGATACGTGTGGAGAAATAAAAGTCGGTCTC 398
Qy 431 ACATTCACCTCTGAGGATCTCGCCAGCGGGTCTCCAGAGGACTTTCGGTGGATGGAAG 490
Db 397 ACTTTACGCGCAGTGGAAACTCG---AGGCTTTGACGAGGAAGCATTCGGAGGATGGAAA 341
Qy 491 CAATCATCTTAGAGCTAGATGCTT 514
Db 340 CATTCGCGCATTAGGAATGCAT 317

RESULT 9

US-10-767-701-11176
; Sequence 11176, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11176
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS15003_1
US-10-767-701-11176

Query Match 22.8%; Score 199.4; DB 17; Length 804;
Best Local Similarity 70.3%; Pred. No. 4.2e-51;
Matches 282; Conservative 0; Mismatches 116; Indels 3; Gaps 1;
Qy 47 GGAGAGGAGGAGCGGAGGAGGACATGGTGCACGCGGAGCGCTGGAGTGTCTGCTGTTGGG 106
Db 142 GGAACACAAGCACCGCGGCAAAACATGGTTTACCGGGAAGCTGGAGGTCTCTCTCTCC 201
Qy 107 GCCAAGGGCTCGAGAACACCGATTACCTCTGTAAACATGATCCGTATGCAATTTCTCAAG 166
Db 202 GCCAAGGGCTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTGATCCTTACA 261
Qy 167 TGCCGTTTCAGGAGCAGAGACAGTATTTGCAACTGGAAAAAGAACTACCCCTGAGTGG 226
Db 262 TGCCGACACAGGAGCAGAAAGCAGCGTCGCAAAATGGAGCAGGAGTGAAGCTGAATGG 321
Qy 227 AATGAAACCTTTATCTTCACTGTCTGACCGGACAAACAGACTTGGTAAATCAAGCTTATG 286
Db 322 AACGAGACCTTCTATCTTCACTGTCTGATGAAACCCCGCAGCTCCATCTCAAGATCATG 381
Qy 287 GACAGTGATACAGCAGCAGCAGATGCTTTGTTGGTGAAGCAACAGTATTCATTCGAAAGCA 346
Db 382 GACAGCGAT---GTCACTAACGATGATTTTGTGGTGAAGCAACCATCTCCCTCTGGAGTT 438
Qy 347 GTGTATATCTGAAAGGAGCATTCCACCACACTCTATAATGTTGTGAAAGGTGAAAAATAC 406
Db 439 GTGTTTCAGGAAGGAGCGCTTCTCCGGCAGTTTCATCCGGTCTGTCAGGAGGAGAAATAC 498
Qy 407 TGGCGGGAATCAAAAGTTGGTCTCACATTCACATTCCTCTGAGGA 447
Db 499 TGGCGGAGATCAAGCTTGGCACTCACCTTCCTCCTCCAGCAGA 539

RESULT 10

US-10-437-963-87038
; Sequence 87038, Application US/10437963
; Publication No. US20040123343A1


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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 122378
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_43093C.1
US-10-425-115-122378

Query Match          20.6%; Score 180.2; DB 18; Length 660;
Best Local Similarity 65.6%; Pred. No. 3.7e-45;
Matches 263; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Qy 47 GGAGAGCGAGGCGGAGGAGGAGATGGTGCACGGGACGCTGGGAAGTCTGCTGTTGGG 106
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Db 39 GGAGATCGAAGAGGAGGAGGAGACATGGTGGCGGGAAGCTGGAGGTGCTGCTGCTCC 98
    |||||

Qy 107 GCCAAGGCGCTCGAAGACACCGATTACCTCTGTAACTGATCGTATGCAATTTCTCAG 166
    |||||
Db 99 GCCAAGGCGCTCGACGATCTCCGATTTCTTCAATAGCATGGACCGGTACGTGATCCTCACC 158
    |||||

Qy 167 TGCCGTTTACAGAGGAGGAGAGAGATTTGCAACTGGAAGAACTACCCCTGAGTGG 226
    |||||
Db 159 TGCCGAGCCACGAGCAGAGAGACCGTCCGATCAGAGCAGGAGGAGCGCTGAGTGG 218
    |||||

Qy 227 AATGAAATCTTTATCTTCTACCTGTGTGACCGGACACAGACTTTGGTAATCAAGCTTATG 286
    |||||
Db 219 AATGAGACCTTCTTCTTCGCCATCTCCGGCGACGCTCCGGAGCTCAGGTCAGATCATG 278
    |||||

Qy 287 GACAGTATACAGCAGCAGCAGATGACTTTTGGTGAAGCAACGATTCATTTGGAAGCA 346
    |||||
Db 279 GACAGCAGCGCCTCTCGGCGAGGACCTCTGTCGGAGAAGCATGCATCCCGCTGGAGCG 338
    |||||

Qy 347 GTGTATCTGAAAGAGGAGATTCACCAACACTCTATAATGTTGTAAGGTGAAATATAC 406
    |||||
Db 339 GTGCTTCAGGAAGGAGCGCTCCCGCGCGCTGCACCGGGTCTGCAAGGAGGAGGTAC 398
    |||||

Qy 407 TGCGGGAAATCAAAGTTGGTCTCACAATTCACCTCTCTGAGGA 447
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Db 399 CGCGGAGAGATCAAGATCGCGCTCACCTTCAACCCCGGAGCA 439
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RESULT 13
US-10-425-114-22597
; Sequence 22597, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22597
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-005-D8_FLI
US-10-425-114-22597

Query Match          20.0%; Score 174.8; DB 16; Length 718;
Best Local Similarity 67.0%; Pred. No. 1.9e-43;
Matches 264; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

Qy 50 GAGCGAGGCGGAGGAGGAGATGGTGCACGGGACGCTGGAAGTCTGCTGTTGGGGCC 109
    |||||
Db 111 GATCGGGGCAAGGAGATAAACATGGTGCACGGGAAGCTGGAGGTCTCTCTGCTCCGCC 170
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Qy 110 AAGGGCGCTCGAGAACACCGATTACCTCTGTAACATGGATCCGTATGCAATTTCTCAAGTGC 169
    |||||
Db 171 AAGGGACTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTGATCTTACCTGC 230
    |||||

Qy 170 CGTTTCAGGAGCAGAGCAGATATTGCAACTGGAAAAAGAACTACCCCTGAGTGAAT 229
    |||||
Db 231 CGCACCCCAAGAGCAGAAAAAGCAGCGTTCGCAATATGGAGCAGGAGCGAGTGAAC 290
    |||||

Qy 230 GAAATCTTATCTTCTACTGTCTGACCGGACCAACAGACTTGGTAATCAAGCTTATGAC 289
    |||||
Db 291 GAGACCTTCTGCTTTCACCGTCTCCGACGACACCCCGCAGCTTCCACCTCAAGATCATGAC 350
    |||||

Qy 290 AGTGATACAGGCACAGCAGATGACTTTGTTGGTGAAGCAACGATTTCATTTGGAAGCAGTG 349
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Db 81 GATCGGGCAAGGAGATAAACATGGTGACCGGAAGCTGGAGGTCTCTCTGCTTCGCC 140
Qy 110 AAGGGCGCTCGAGAACACCGATTACCTCTGTAAACATGATCGTATGCAATTTCTCAAGTGC 169
    |||||
Db 141 AAGGACTCGAGNACACCGATTTCTCAATAACATGAGACCCCTTCGTGATCTTACCTGC 200
    |||||

Qy 170 CGTTTCAGGAGCAGAGCAGATATTGCAACTGGAAGAACTACCCCTGAGTGAAT 229
    |||||
Db 201 CGCACCCCAAGAGCAGAAAAAGCAGCGTTCGCAATATGGAGCAGGAGCGCCGAAATGGAAC 260
    |||||

Qy 230 GAAATCTTATCTTCTACTGTCTGACCGGACCAACAGACTTGGTAATCAAGCTTATGAC 289
    |||||
Db 261 GAGACCTTCTGCTTTCACCGTCTCCGACGACACCCCGCAGCTGCAAGATCATGAC 320
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Qy 290 AGTGATACAGCAGCAGCAGATGACTTTGTTGGTGAAGCAACGATTTCCATTTGGAAGCAGTG 349
    |||||
Db 321 AGCA---CCTCACAACGAGATTTCTGTCGGCAGCAACCATCCCCCTGGAGCGCGTG 377
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Qy 350 TATACTGAAAGGAGCATTCCACCAACTCTATAATGTTGTAAGGTGAAAAATATCTGC 409
    |||||
Db 378 TTTCAGGAAGGAGCGCTTCCCGCGGTTTCAACCGGTCTGTCAGGAGGAGGAGTACTGC 437
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Qy 410 GGGGAATCAAAGTTGGTCTCACATTCACCTCCTG 443
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Db 438 GGAGAGGTCAAGCTCGCGCTCACCTTCACTCCAG 471
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RESULT 14
US-10-425-114-2939
; Sequence 2939, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2939
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700237789_FLI
US-10-425-114-2939

Query Match          20.0%; Score 174.8; DB 16; Length 741;
Best Local Similarity 67.0%; Pred. No. 2e-43;
Matches 264; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

Qy 50 GAGCGAGGACGGAGGAGGAGATGGTGCACGGGACGCTGGAAGTCTGCTGTTGGGGCC 109
    |||||
Db 111 GATCGGGCAAGGAGATAAACATGGTGCACGGGAAGCTGGAGGTCTCTCTGCTCCGCC 170
    |||||

Qy 110 AAGGGCGCTCGAGAACACCGATTACCTCTGTAACATGGATCCGTATGCAATTTCTCAAGTGC 169
    |||||
Db 171 AAGGGACTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTGATCTTACCTGC 230
    |||||

Qy 170 CGTTTCAGGAGCAGAGCAGATATTGCAACTGGAAAAAGAACTACCCCTGAGTGAAT 229
    |||||
Db 231 CGCACCCCAAGAGCAGAAAAAGCAGCGTTCGCAATATGGAGCAGGAGCGAGTGAAC 290
    |||||

Qy 230 GAAATCTTATCTTCTACTGTCTGACCGGACCAACAGACTTGGTAATCAAGCTTATGAC 289
    |||||
Db 291 GAGACCTTCTGCTTTCACCGTCTCCGACGACACCCCGCAGCTTCCACCTCAAGATCATGAC 350
    |||||

Qy 290 AGTGATACAGGCACAGCAGATGACTTTGTTGGTGAAGCAACGATTTCATTTGGAAGCAGTG 349
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Db 351 AGCGA---CCTCACCACGACGATTTCGTGGCGAAGCAACCATCCCTCTGGAGGCCGTG 407
QY 350 TATACTGAAGAGGATTCACCAACTCTATATGTGTGAAAGGTGAAAAATACTGC 409
Db 408 TTTCAGGAAGGACGCTTCCCGCGCGGTTTCCCGGTCGTCAAGGAGGAGAGTACTGC 467
QY 410 GGGGAAATCAAAGTTGGTCTCACATTCACTCCTG 443
Db 468 GGAGAGGTCAAGCTCGCGCTCACCTTCACTCCAG 501

RESULT 15

US-10-425-115-106431
; Sequence 106431, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 106431
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_28567C.1
US-10-425-115-106431

Query Match 19.8%; Score 173.6; DB 18; Length 1294;
Best Local Similarity 67.3%; Pred. No. 6.5e-43;
Matches 261; Conservative 0; Mismatches 124; Indels 3; Gaps 1;
QY 56 GGAGCGGAGGAGGACATGGTGCACGGGAGCTGGAGTGTCTGCTGGGGCCCAAGGGC 115
Db 665 GGGAGGAGATAAATGTTGACGGGAGCTGGAGTGTCTGCTGCTCCGCCAAGGGA 724
QY 116 CTCGAGAACCGGATACCTCTGTAAATGGATCCGTATGCAATTCCTCAAGTCCCGTTCA 175
Db 725 CTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTATCCTTACCTGCCGACC 784
QY 176 CAGGAGCAGAGGAGGATTTGCAACTGGAAAGGAACTACCCCTGAGTGGAAATGAAAC 235
Db 785 CAAGAGCAGAAAGCAGCGTCCGCAATGGAGCAGGAAGCGAGCCCGAGTGAACGAGACC 844
QY 236 TTTATCTTCACTGTGTCTGACCGCAACAGACTTCGTAATCAAGCTTATGGACAGTGAT 295
Db 845 TTGCTCTTCACTGCTCCGAGGACACCCGCGAGCTCCACCTCAAGATCATGGACAGCGAT 904
QY 296 ACAGGCACAGCAGATGACTTTGTGTGTAAGCAACGATTCCATTGGAAGCAGTGTATACT 355
Db 905 ---CTCACCACGACGATTTCGTGCGGCGAAGCAACCATCCCTCGAGGCCGTGTTTCA 961
QY 356 GAAAGGAGCATTCACCAACACTCTATATGTGTGAAAGGTGAAAAATACTGCGGGGAA 415
Db 962 GAAAGGAGCCTTCCCGCGGTTTCCCGGTTTCCCGGTTTCCCGGTTTCCCGGTTTCCCG 1021
QY 416 ATCAAGTGGTCTCACATTCACTCCTG 443
Db 1022 GTCAAGCTCGCGTCACTTCACTCCAG 1049

Search completed: January 8, 2005, 11:49:11
Job time : 588 secs

Qy	373	AACACTCTATAATGTTGTGAAGGTGAAATAATCTCGGGGAAATCAAAGTTGGTCTCAC	432
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Qy	433	ATTCACTCTCTGAGGATCTCGCCAGCGGGGTCTCCAGAG---	489
Db	361	GTTCACTCCAGAGGATGATCGCGATCGGGGTTTATCTGAGGAAGACATTGGTGGATGGAA	420
Qy	490	GCAATCATCTT-----AGAGCTAGATGCTTTAAGGGTGCACCAGACAGCGACAATTC	544
Db	421	GCAGTCATCTTGAGGAAGACAGATACCTTTGATGTGCACTGCATCGCTATGGTAAGTC	480
Qy	545	ATGCGCTTGGAGC	557
Db	481	GTGTGCTGGNACC	493

Search completed: January 8, 2005, 09:17:44
 Job time : 3413 secs

Qy 481 TGGATGGAAGCAATCATCTTA 501
 Db 345 TGGATGGAAGCAATCTCGTTA 325

RESULT 14
 CF335095 540 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--04-K06.bi AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--04-K06, mRNA sequence.
 CF335095
 CF335095.1 GI:33818529
 EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 540)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--04-K06"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

ORIGIN
 Query Match 32.4%; Score 284.2; DB 6; Length 540;
 Best Local Similarity 77.9%; Pred. No. 4.8e-73;
 Matches 356; Conservative 0; Mismatches 98; Indels 3; Gaps 1;

Qy 47 GGAGCGGAGGAGCGGAGGACATGGTGCACGGGACGCTGGAGTGTCTGCTGGG 105
 Db 3 GGGCGCGGGGAGCTGGGAACTGGTGCAGGGACGCTCGAGGTGCTGCTCGGA 62

Qy 107 GCCAAGGGCTCGAGAACCCGATTACTCTGTAAACATGGATCGGTATGCAATTC 166
 Db 63 GCCAAGGGCTCGAGAACCCGATTACTCTGTAAACATGGATCGGTATGCAATTC 122

Qy 167 TCCCGTTACAGGAGCAGAGCAGTATTGCAACTGGAAAGAACTACCCCTGAGTGG 225
 Db 123 TCCCGTTCCAGAGCAGAGCAGGTTGCGTCAAGTAAAGCTGACCCCTGAAATGG 182

Qy 227 AATGAAACCTTTATCTTCTACCTGTCTGACCGGACAAACAGACTTTGGTAATCAAGCTTATG 286
 Db 183 AACGAAACCTTTATGTTTCCAGGCTCACTCAACAGCTACAGAGCTCATCATCAAGTTGATG 242

Qy 287 GACAGTATACGACGACGACGATGCTTTGGTGGAGCAACGATTCATTCGGAAGCA 346
 Db 243 GACAGTACGATGCGCAGGATGATGATTTTGGTGGAGCAACGATTCATTCGGAAGCA 302

Qy 347 GTGTATACTGAAGGAGCATTCACCAACACTCTATATGTTGTGAAGGTGAAAAATAC 406
 Db 303 ATCTATACAGAGGAGCATACCCCAACTGTTTATATGTTGTGAAGGAGAAATAC 362

Qy 407 TCGGGGAAATCAAAGTTGGTCTCACATTCACTCTGAGGATACCTCCACGCGGGTCTC 466
 Db 363 CGTGGAAATCAAAGTGGCGCTGACGTTCACTCCAGAGGATGATCGGATCGGGTTTA 422

Qy 467 CCAGAG---GACATTCGGTGGATGGAACCAATCATCTT 500
 Db 423 TCTGAGGAAGACATTTGGTGGATGGAACGATCATCTT 459

RESULT 15
 D23846
 LOCUS RICR0374A Rice root Oryza sativa (japonica cultivar-group) cDNA
 DEFINITION clone R0374, mRNA sequence.
 D23846 AU031663
 ACCESSION D23846.2 GI:15072279
 VERSION EST.
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Minobe, Y. and Sasaki, T.
 TITLE Rice cDNA from root
 JOURNAL Unpublished (1995)
 COMMENT On Dec 2, 1993 this sequence version replaced gi:427711 gi:3767636.
 Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 PROJECT = RGP.

FEATURES
 source
 1..676
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="R0374"
 /clone_lib="Rice root"
 /notes="Prepared from seedling root."

ORIGIN
 Query Match 31.9%; Score 279.4; DB 7; Length 676;
 Best Local Similarity 75.9%; Pred. No. 1.4e-71;
 Matches 374; Conservative 0; Mismatches 111; Indels 8; Gaps 2;

Qy 73 GGTGCAGCGGACCTGGAGTGTCTGCTGGGGCCAGGGCTCGAGAACCCGATTA 132
 Db 1 GGTGCAGCGGACCTCGAGTGTCTGCTCGGACCAAGGGCTCGAGAACCCGACTA 60

Qy 133 CCTCTGTAAATGATCCGTTATGCAATTTCTCAAGTCCGTTTACAGAGCAGAGAGCAG 192
 Db 61 CCTGTGCAATGAGACCCGTACGGGTTCTCAATGCCGCTCGCAGAGGAGAGAGCAG 120

Qy 193 TATTGCACTGGAAGGAACTACCCCTGAGTGGAAATGAAAATTTATCTTCTACTGTGC 252
 Db 121 CGTTGCGTCAGGTAAAGGATCTGACCTGAAATGGAACGAAACCTTTATGTTTCAGCGTCAC 180

Qy 253 TGACCGGACAAACAGACTTGGTATCAAGCTTATGGACAGTGATACAGGCACACGATGA 312
 Db 181 TCACAACGCTACAGAGCTCATCATCAAGTTGATGGACAGTGACAGTGGCAGCGATGATGA 240

Qy 313 CTTTGTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATCTACTGAAAGGAGCATTCCACC 372
 Db 241 TTTTGTGGAGAGCAACGATTTCTTTGGAGCAATCTATACAGAGGAGGACATACCCCC 300

Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Clas: sheared ends.

FEATURES

Location/Qualifiers
1..816
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0639G14"
/clone_lib="ZM_0.7.1.5_KB"
/note="Vector: pBGSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 34.7%; Score 304.4; DB 9; Length 816;
Best Local Similarity 99.7%; Pred. No. 5.2e-79;
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 571 GTACTTCATGCTPAATGAGAAATTCATTCGATTGGCTTCTTTGATTTGTTTCAGAGAAG 630
Db 1 GTACTTCATGCTPAATGAGAAATTCATTCGATTGGCTTCTTTGATTTGTTTCAGAGAAG 60
QY 631 TGTATTATTAGTGGTTTCAACAAAATAATAGCTCCATATTCGCTCTATATCCCGTATTGGAAA 690
Db 61 TGTATTATTAGTGGTTTCAACAAAATAATAGCTCCATATTCGCTCTATATCCCGTATTGGAAA 120
QY 691 TTCTAAGCCGTTTCTGTGATTCTGCTTACACAGAAGTTTGTCTAGTTCCTACCTAC 750
Db 121 TTCTAAGCCGTTTCTGTGATTCTGCTTACACAGAAGTTTGTCTAGTTCCTACCTAC 180
QY 751 GCTTTTTTTTGAAGTTTTCAGTGGAAACATCTTGTGTTTCAACGTTTGGGAGGTGTAGGC 810
Db 181 GCTTTTTTTTGAAGTTTTCAGTGGAAACATCTTGTGTTTCAACGTTTGGGAGGTGTAGGC 240
QY 811 CAGTAATCTGCAAGAAAGGAATATTTCCCTTGCAGCAACATTTGTTTGTGATCCTT 870
Db 241 CAGTAATCTGCAAGAAAGGAATATTTCCCTTGCAGCAACATTTGTTTGTGATCCTT 300
QY 871 GAAAAA 876
Db 301 GAACAA 306

RESULT 11

CB674853
LOCUS
DEFINITION
OSJNEA10C10.f OSJNEE Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEE10C10.5', mRNA sequence.
CB674853
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 751)
Jantaseviyavat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA

Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 Row: C Column: 10
Seq primer: gta aac cga cgg cca gtcg.

FEATURES

Location/Qualifiers
1..751
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEE10C10"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEE"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN

Query Match 33.3%; Score 291.6; DB 6; Length 751;
Best Local Similarity 74.9%; Pred. No. 3.3e-75;
Matches 394; Conservative 0; Mismatches 124; Indels 8; Gaps 2;
QY 47 GGAAGCGAGGAGCGGAGGAGGACATGGTSCACGGGACGCTGGAAGTGTCTGCTGTTGGG 106
Db 48 GGGCGCGGGGAGCTGGGGAAGATGGTGCAGGGAGCGCTCGAGGTGCTGCTGCTCGGA 107
QY 107 GCCAAGGGCTTCAGAACACCGATTACCTCTGTAACTGGATCCGTATGCAATTCCTCAAG 166
Db 108 GCCAAGGGCTTCAGAACACCGATTACCTCTGTAACTGGATCCGTATGCAATTCCTCAAG 167
QY 167 TGGCGTTTCAGAGGAGGAGGACGATTTGCAACTGGAAAAGGAACTACCCCTGAGTGG 226
Db 168 TGGCGCTCGCAGGAGGAGGAGGAGCGGTTGCTCAGGTAAAGGATCTGACCTGAATGG 227
QY 227 AATGAAACCTTTATCTTCACTGTGTGACCGGACCAACAGACTTGGTAAATCAAGCTTATG 286
Db 228 AACGAAACCTTTATGTTACGCGTCACTCAACCGCTACAGAGCTCATCATCAAGTTGATG 287
QY 287 GACAGTGATACAGGACGACGAGTGTGTTGGTGAAGCAACGATTCATTCGGAAGCA 346
Db 288 GACAGTGATACAGGACGAGTGTGTTGGTGAAGCAACGATTCATTCGGAAGCA 347
QY 347 GTGTATCTGAAAGGAGGACATTCACCAACACTCTATAATGTTGTGAAAGGTGAAAATAC 406
Db 348 ATCTATACAGAGGAGGACATACCCCACTGTTTATATGTTGTGAAGAGAGATAC 407
QY 407 TGGCGGGAATCAAAATGTTGTTCTACATTCCTCTGAGGATACTGCCAGCGGGTCTC 466
Db 408 CGTGGAGAAATCAAAAGTGGGCTGAGCTTCACTCCAGAGGATGATCGCATCGGGTTTA 467
QY 467 CCAGAG--GACTTCGTTGGATGGAGCAATCATCTT-----AGACTAGATGCTTTAAG 518
Db 468 TCTGAGGAAGACATTTGGTGGATGGAAGCAGTCACTTTGAGGAAGAGAGAGACTTTGAT 527
QY 519 GTTGCAACAGAGACAGCGACCAATTCATGCGTTGGAGGCTTCAGC 564
Db 528 GTGCACTGCATCGCTATGTTAAGTCTGTTGTTGAGGAGCTGGAAC 573

RESULT 12

CA755886
LOCUS
DEFINITION
CA755886
622 bp mRNA linear EST 27-NOV-2002
BR030030000 PLATE_E11_85_086.ab1 OA Oryza sativa (japonica
cultivar-group) cDNA clone BR030030000 PLATE_E11_85_086.ab1 similar
to elicitor-responsive gene 3 [imported] - rice
gi|3603473|gb|AAC35866.1| (AF090698) elicitor-responsive gene-3
[Oryza sativa] [Oryza sativa (indica cultivar-group)]
gi|21998839|dbj|BAC06444.1| (AB060729) RPP16 [Oryza sativa]

ORIGIN /clone_lib="GeneTag2"

Query Match 42.0%; Score 367.8; DB 6; Length 371;
 Best Local Similarity 99.5%; Pred. No. 5e-98; 2; Indels 0; Gaps 0;
 Matches 369; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 146 GATCCGATGCAATTTCTCAAGTCCCGTTTCACAGGAGCAGAGCAGTATTTGCAACTGGA 205
 DB 1 GATCCGATGCAATTTCTCAAGTCCCGTTTCACAGGAGCAGAGCAGTATTTGCAACTGGA 60

QY 206 AAGGAACTACCCCTGAGTGAATGAAACTTTATCTCTGCTGTGTCAGCCGCAACA 265
 DB 61 AAGGAACTACCCCTGAGTGAATGAAACTTTATCTCTGCTGTGTCAGCCGCAACA 120

QY 266 GACTTCGTATCAAGCTTATGGACAGTGATACAGGACACAGCAGATCACTTTGCTGGA 325
 DB 121 GACTTCGTATCAAGCTTATGGACAGTGATACAGGACACAGCAGATCACTTTGCTGGA 180

QY 326 GCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTCACCAACACTCTATAAT 385
 DB 181 GCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTCACCAACACTCTATAAT 240

QY 386 GTTGTGAAGGTGAAATAATCTCGGGGAAATCAAAAGTTGGTCTCAATTCATCTCTAG 445
 DB 241 GTTGTGAAGGTGAAATAATCTCGGGGAAATCAAAAGTTGGTCTCAATTCATCTCTAG 300

QY 446 GATACCTGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAGCAATCATCTTAGGC 505
 DB 301 GATACCTGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAGCAATCATCTTAGGC 360

QY 506 TAGATGCTTTA 516
 DB 361 TAGATGCTTTA 371

RESULT 9
 BF482583 746 bp mRNA linear EST 06-DEC-2000
 LOCUS WHE2301-2304_G04_G04ZS Wheat pre-anthesis spike cDNA library
 DEFINITION Triticum aestivum cDNA clone WHE2301-2304_G04, mRNA sequence.
 ACCESSION BF482583
 VERSION BF482583.1 GI:11565973
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 746)
 AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y.Y., Iazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
 TITLE The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@pw.ars.gov
 Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
 Seq primer: Strategene SK primer.
 Location/Qualifiers
 FEATURES
 source 1..746
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE2301-2304_G04_G04"

/tissue_type="Spike before anthesis"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /clone_lib="Wheat pre-anthesis spike cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the T3 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 38.3%; Score 335.8; DB 2; Length 746;
 Best Local Similarity 84.0%; Pred. No. 2.2e-88;
 Matches 379; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 50 GAGCGAGGAGCGGAGGAGCATGGTGACGGGAGCGTGGAAAGTGTCTGCTTGGGGCC 109
 DB 52 GACTCAGGAGGAGGAGATCGATGGTGACGGAACTGGAGGTGTCTGCTCGCGGCC 111

QY 110 AAGGGCCTCGAGAACACCGATTACCTCTGTAAATGATCCGATGCAATTTCTCAAGTGC 169
 DB 112 AAGGGCCTCGAGAACACCGATTACCTCTGCAATATGGATCCGTACGCACCTTCTCAATATGC 171

QY 170 CGTTACAGGAGCAGAGCAGTATTGCACTGTAACTGGAAGGAACTACCCCTGAGTGGAAAT 229
 DB 172 CGCTCGCAGGAGCAGAGGAGCATTTGCATCAGGCAAAAGGTAGTAACCTCGAATGGAAC 231

QY 230 GAAAACTTTATCTCACTGTCTGACCGGACACAGACTTGGTAATCAAGCTTATGGAC 289
 DB 232 GAAAGCTTTGTCTTACCGTGTACAGCAATGTACGAGCTGGTGTCAAGCTTATGGAC 291

QY 290 AGTGATACAGGCACAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTTGGAAGCAGTG 349
 DB 292 ACGGACTCGGGCACATCGGACGACTTCGTTGGTGAAGCAACGATTCCTTTGGAAGCAGTT 351

QY 350 TATACGTAAGAGCAGATTCACCAACACTCTATATGTTGTGAAAGGTGAAAAATCTGTC 409
 DB 352 TATACCGAAGGAGCAGATTCACCAACAGTTTAAATGTTGTGAAAGGTGAACACTACTGT 411

QY 410 GGGGAAATCAAGTTGGTCTCACTCTGAGGATACCTCGCCAGCGGGTCTCTCCCA 469
 DB 412 GGAGAAATCAAGTGGTCTCACTCTGAGGATACCTCGCCAGGATACCTCGCCAGCGGGTCTCTCC 471

QY 470 GAGGACTTCGGTGGATGGAAGCAATCATCTT 500
 DB 472 GAAGACTTCGGTGGTGGAAACAATCGCATT 502

RESULT 10
 CG237557 816 bp DNA linear GSS 22-AUG-2003
 LOCUS OGYBD43TH_ZM_0_7_1.5_KB_Zea_mays genomic clone ZMMBma0639G14,
 DEFINITION genomic survey sequence.
 ACCESSION CG237557
 VERSION CG237557.1 GI:34137443
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 816)
 AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Other_GSSs: OGYBD43TV

CoT selected genomic DNA library"

ORIGIN

Query Match 49.4%; Score 432.8; DB 9; Length 977;
Best Local Similarity 98.4%; Pred. No. 2.9e-117;
Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 433 ATTCATCTCCTGAGGATCTCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 492
Db 12 ATTCCTTTATGTAGGATCTCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 71

QY 493 ATCATCTTAGCTAGATGCTTTAAGGGTGACACAGACAGCAATTCATCGCGTT 552
Db 72 ATCATCTTAGCTAGATGCTTTAAGGGTGACACAGACAGCAATTCATCGCGTT 131

QY 553 GGAGCCTTCAGCGGTGAGTACTTCATCTAATGAGAAATTCATTCGATTTGGCTCTTT 612
Db 132 GGAGCCTTCAGCGGTGAGTACTTCATCTAATGAGAAATTCATTCGATTTGGCTCTTT 191

QY 613 TGATTTGTTTCAGAGAGTGTATTAGTGTAGTTTCAACAAAAATAGCTCCATATTGCTC 672
Db 192 TGATTTGTTTCAGAGAGTGTATTAGTGTAGTTTCAACAAAAATAGCTCCATATTGCTC 251

QY 673 TATATCCGTTATTGAAATCTTAAGCGGCTTTGTGATTTACTGCTTCAACAAAGAGTTT 732
Db 252 TATATCCGTTATTGAAATCTTAAGCGGCTTTGTGATTTACTGCTTCAACAAAGAGTTT 311

QY 733 GCTTCTAGTCCCACTACGCTTTTGTGAGTTTGTGAGTGGAGACATCTTTGCTTCAAC 792
Db 312 GCTTCTAGTCCCACTACGCTTTTGTGAGTTTGTGAGTGGAGACATCTTTGCTTCAAC 371

QY 793 GTTTGGGAGGTGAGGACGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACA 852
Db 372 GTTTGGGAGGTGAGGACGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACA 431

QY 853 TTGTTTTTGTGATCCCTTGA AAAA 876
Db 432 TTGTTTTTGTGATCCCTTGAACAA 455

RESULT 7

LOCUS BZ538974 721 bp DNA linear GSS 16-DEC-2002
DEFINITION OGAEC73TC ZM2 0.7 1.5 KB Zea mays genomic clone ZMBMa0040N01,
genomic survey sequence.

ACCESSION BZ538974
VERSION BZ538974.1 GI:27087410
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 721)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..721
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

FEATURES
source

/clone="ZMBMa0040N01"
/clone_lib="ZM2 0.7 1.5 KB"
/note="vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 49.2%; Score 431.4; DB 8; Length 721;
Best Local Similarity 99.8%; Pred. No. 6.9e-117;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 444 AGGATATCCGACGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATCATCTTAGA 503
Db 712 AGGATATCCGACGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATCATCTTAGA 653

QY 504 GCTAGATGCTTTAAGGGTGACACAGACAGCAATTCATCGCTTCGAGCCTTCAG 563
Db 652 GCTAGATGCTTTAAGGGTGACACAGACAGCAATTCATCGCTTCGAGCCTTCAG 593

QY 564 CCGTCGAGTACTTCATCTAATGAGAAATTCATTCGATTTGGCTTCTTTGATTTGTTCA 623
Db 592 CCGTCGAGTACTTCATCTAATGAGAAATTCATTCGATTTGGCTTCTTTGATTTGTTCA 533

QY 624 GAAGAGTGTATTAGTGTAGTTTCAACAAAAATAGCTCCATATTGCTCTATATCCGTA 683
Db 532 GAAGAGTGTATTAGTGTAGTTTCAACAAAAATAGCTCCATATTGCTCTATATCCGTA 473

QY 684 TTGGAATTTCTAAGCGGCTTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGT 743
Db 472 TTGGAATTTCTAAGCGGCTTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGT 413

QY 744 CCATCTAGCTTTTGTGAAAGTTTTCAGTGGAAACATCTTTGTGTTCAACGTTTGGGAGG 803
Db 412 CCATCTAGCTTTTGTGAAAGTTTTCAGTGGAAACATCTTTGTGTTCAACGTTTGGGAGG 353

QY 804 TGTAGGCCAGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACATGTTTTTGT 863
Db 352 TGTAGGCCAGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACATGTTTTTGT 293

QY 864 GATCCTTGA AAAA 876
Db 292 GATCCTTGAACAA 280

RESULT 8

LOCUS CD950747 371 bp mRNA linear EST 15-JUL-2003
DEFINITION SAS_153 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION CD950747
VERSION CD950747.1 GI:32798511
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 371)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..371
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"

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493 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGCAGCAGCAATTCATGCGCTT 552
|||
425 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGCAGCAGCAATTCATGCGCTT 484
|||
553 GGAGCCTTCAGCGCTCGAGTACTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 612
|||
485 GGAGCCTTCAGCGCTCGAGTACTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 544
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613 TGATTTGTTTCAAGAAGTGTATTAAGTGTAGTGTTCACAAAAAATAGTCCATATTTGCTC 672
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545 TGATTTGTTTCAAGAAGTGTATTAAGTGTAGTGTTCACAAAAAATAGTCCATATTTGCTC 604
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673 TATATCCCGTATTTGGAATTTCTAAGGCCGTTTGTGATTAAGTGTTCACAAAAAATAGTCCATATTTGCTC 732
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605 TATATCCCGTATTTGGAATTTCTAAGGCCGTTTGTGATTAAGTGTTCACAAAAAATAGTCCATATTTGCTC 664
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733 GCTTCTAGTTCACACTACGCTTTTTTTTGAAGTTTGTGAGTGAACATCTTTGTTGTTCAAC 792
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665 GCTTCTAGTTCACACTACGCTTTTTTTTGAAGTTTGTGAGTGAACATCTTTGTTGTTCAAC 724
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793 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATAATTTCCCTTGCGAGCAACA 852
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725 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATAATTTCCCTTGCGAGCAACA 784
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853 TTGTTTTTTTGTGATCCTTGAAAAA 876
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785 TTGTTTTTTTGTGATCCTTGAACAA 808
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RESULT 5
CG372852
LOCUS
DEFINITION
CG372852
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 896)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGI:DS04TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .896
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0739A07"
/clone_lib="ZM 0.7 1.5 kb"
/notes="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

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FEATURES
source
1. .896
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0739A07"
/clone_lib="ZM 0.7 1.5 kb"
/notes="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

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ORIGIN
Query Match 49.4%; Score 432.8; DB 9; Length 896;

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Best Local Similarity 98.4%; Pred. No. 2.8e-117;
Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 433 ATCTACTCTTAGAGTACTCGCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 492
|||
60 ATCTCTTATGTAGGATACTCGCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 119
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493 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGCAGCAGCAATTCATGCGCTT 552
|||
120 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGCAGCAGCAATTCATGCGCTT 179
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553 GGAGCCTTCAGCGCTCGAGTACTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 612
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180 GGAGCCTTCAGCGCTCGAGTACTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 239
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613 TGATTTGTTTCAAGAAGTGTATTAAGTGTAGTGTTCACAAAAAATAGTCCATATTTGCTC 672
|||
240 TGATTTGTTTCAAGAAGTGTATTAAGTGTAGTGTTCACAAAAAATAGTCCATATTTGCTC 299
|||
673 TATATCCCGTATTTGGAATTTCTAAGGCCGTTTGTGATTAAGTGTTCACAAAAAATAGTCCATATTTGCTC 732
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300 TATATCCCGTATTTGGAATTTCTAAGGCCGTTTGTGATTAAGTGTTCACAAAAAATAGTCCATATTTGCTC 359
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733 GCTTCTAGTTCACACTACGCTTTTTTTTGAAGTTTGTGAGTGAACATCTTTGTTGTTCAAC 792
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360 GCTTCTAGTTCACACTACGCTTTTTTTTGAAGTTTGTGAGTGAACATCTTTGTTGTTCAAC 419
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793 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATAATTTCCCTTGCGAGCAACA 852
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420 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATAATTTCCCTTGCGAGCAACA 479
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853 TTGTTTTTTTGTGATCCTTGAAAAA 876
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480 TTGTTTTTTTGTGATCCTTGAACAA 503
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RESULT 6
CG171937
LOCUS
DEFINITION
CG171937
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 977)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFKS52TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .977
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0672J07"
/clone_lib="ZM 0.6 1.0 kb"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

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1. .977
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0672J07"
/clone_lib="ZM 0.6 1.0 kb"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

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QY 537 GACAATTCATGCGTTGGAGCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGAAATTCAT 596
Db 229 GACAATTCATGCGCTTGGAGCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGAAATTCAT 170
QY 597 TCGATTGGCTCTCTTTGATGTTTCAGAGAAGTGTATTAGTGAAGTTTCAACAAAAA 656
Db 169 TCGATTGGCTCTCTTTGATGTTTCAGAGAAGTGTATTAGTGAAGTTTCAACAAAAA 110
QY 657 TAGCTCCATATTGCTCTATATCCGTAATCCGTAATGGAATTCCTAAGCCGTTTGTGATTACTGCT 716
Db 109 TAGCTCCATATTGCTCTATATCCGTAATGGAATTCCTAAGCCGTTTGTGATTACTGCT 50
QY 717 TACAACAAGAGTTTTCCTCTAGTCTCCCACTA 749
Db 49 TACAACAAGAGTTTTCCTCTAGTCTCCCACTA 17

RESULT 3
AWS19994/c
LOCUS 66058D08.x2 660 - Mixed stages of anther and pollen Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AWS19994
VERSION AWS19994.1 GI:7162372
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 534)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 660058 row: D column: 08.
FEATURES
source
location/Qualifiers
1..534
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/tissue_type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
/lab_host="XfOLR"
/clone_lib="660 - Mixed stages of anther and pollen"
/notes="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
Site_2: XhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin."

ORIGIN
Query Match 59.2%; Score 518.4; DB 2; Length 534;
Best Local Similarity 99.4%; Pred. No. 7.3e-143;
Matches 531; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 316 TGTGTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCAAC 375
Db 534 TGTGTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCATC 475

QY 376 ACTCTATATGTTGGAAGTGAATAATCTCGGGGAATCAAGTTGCTCTCACATT 435
Db 474 ACTCTATATGTTGGAAGTGAATAATCTCGGGGAATCAAGTTGCTCTCACATT 415

QY 436 CACTCTCTGAGGATCTCGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATC 495
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Db 414 CACTCTGAGGATCTCGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATC 355
QY 496 ATCTTAGAGCTAGATGCTTTAAGGGTGACACAGAGCAGCAGCACAATTCATCGGCTTGA 555
Db 354 ATCTTAGAGCTAGATGCTTTAAGGGTGACACAGAGCAGCAGCACAATTCATCGGCTTGA 295
QY 556 GCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGAAATTCATTCGATTTGGCTTCTTTTGA 615
Db 294 GCCTTCAGCCGTCGAGTACTTCATGCTAATGCAGAAATTCATTCGATTTGGCTTCTTTTGA 235
QY 616 TTGTTTTCAGAGAAGTGTATTAGTGAAGTTTCAACAAAAAATAGCTCCATATTGCTCTAT 675
Db 234 TTGTTTTCAGAGAAGTGTATTAGTGAAGTTTCAACAAAAAATAGCTCCATATTGCTCTAT 175
QY 676 ATCCCGTATTGGAATTCCTAAGCCGTTTGTGATTACTGCTTACACAGAGAAGTTTGGCT 735
Db 174 ATCCCGTATTGGAATTCCTAAGCCGTTTGTGATTACTGCTTACACAGAGAAGTTTGGCT 115
QY 736 TCTAGTTCCCACTACGSC--TTTTTTGAAGTTTTCAGTGGACATCTTTGTGTTCAACG 793
Db 114 TCTAGTTCCCACTACGCTTTTTTTTGAAGTTTTCAGTGGACATCTTTGTGTTCAACG 55
QY 794 TTTGGGAGGTGTAGGCCAGTAAATCTGCAAGAAAGGAATAATTTCCCTTGCAG 847
Db 54 TTTGGGAGGTGTAGGCCAGTAAATCTGCAAGAAAGGAATAATTTCCCTTGCAG 1

RESULT 4
CG280271 860 bp DNA linear GSS 25-AUG-2003
OG0GP83TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0713N22,
genomic survey sequence.
CG280271 GI:34194390
VERSION CG280271.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 860)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG0GP83TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
source
location/Qualifiers
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/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0713N22"
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methylation filtered genomic DNA library"

ORIGIN
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Best Local Similarity 98.4%; Pred. No. 2.8e-117;
Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 433 ATTCATCTCTGAGGATCTCGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 492
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[illegible]

RESULT 2	589 bp	linear	EST 29-MAY-2001
LOCUS	589 bp	linear	EST 29-MAY-2001
DEFINITION	589 bp	linear	EST 29-MAY-2001
ACCESSION	589 bp	linear	EST 29-MAY-2001
VERSION	589 bp	linear	EST 29-MAY-2001
KEYWORDS	589 bp	linear	EST 29-MAY-2001
SOURCE	589 bp	linear	EST 29-MAY-2001

ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1. (bases 1 to 589)
TITLE	Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.
JOURNAL	Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
COMMENT	On May 25, 2001 this sequence version replaced gi:14209197. Contact: Patrick S. Schnable Schnable Laboratory Iowa State University G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975 Fax: 515-294-2299 Email: schnable@iastate.edu PCR Primers FORWARD: T7-1 (AA TAC GAC TCA CTA TAG) BACKWARD: T3 (ATT AAC CCT CAC TAA AG) Seq primer: primer T3 (ATT AAC CCT TAA AG).

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FEATURES             source
Location/Qualifiers
1..589
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/cultivar="B73"
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/clone="MEST41-A12"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/clone_lib="ISUM4-TN"
/note="Vector: p7T73PAC; Site 1: EcoRI; Site 2: NotI;
ds-cDNA molecules were generated as follows_First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'-
AATCGAAGATTCGCGCCGACGGAATTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the p7T73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

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Research 6: 791-806, 1996).

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	Query Match	65.0%;	Score 569.8;	DB 4;	Length 589;
	Best Local Similarity	99.7%;	Pred. No. 3.6e-158;		
	Matches 571;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
177	AGGAGCAGACAGCAGATATTC	CAACTG	GAAAGGAAC	TACCCCTCGAGTGGGAATG	AAACT 236
589	AGGAGCAGACAGCAGATATTC	CAACTG	GAAAGGAAC	TACCCCTCGAGTGGGAATG	AAACT 530
237	TTATCTTCACCTGTGTCTGAC	CGGCAAC	CAGACACTTGG	TAACTCAAGCTTATGAC	CAGTGATA 296
529	TTATCTTCACCTGTGTCTGAC	CGGCAAC	CAGACACTTGG	TAACTCAAGCTTATGAC	CAGTGATA 470
297	CAGGCACAGCAGATGAC	CTTTTGTGGTGAAGCAAC	CGATTC	CAATTTGGAAGCAGTGT	TACTG 356
469	CAGGCACAGCAGATGAC	CTTTTGTGGTGAAGCAAC	CGATTC	CAATTTGGAAGCAGTGT	TACTG 410
357	AAAGGAGCATTTCCACCAAC	ACTCTTATATGTTGTGAAG	GGTGAAAAATAT	TCGCGGGGAAA	416
409	AAAGGAGCATTTCCACCAAC	ACTCTTATATGTTGTGAAG	GGTGAAAAATAT	TCGCGGGGAAA	350
417	TCAAAGTTGGTCTCACAT	TTCAC	TCTCCTGAGGATA	CTCGCCAGCGGGGTCT	CCGAGGACT 476
349	TCAAAGTTGGTCTCACAT	TTCAC	TCTCCTGAGGATA	CTCGCCAGCGGGGTCT	CCGAGGACT 290
477	TCGGTGGATGAAGGAAT	TCATCTTTAGAGCTAGAT	GTCTTTTAAGGGTGC	NCNCAGACACAGC	536
289	TCGGTGGATGAAGGAAT	TCATCTTTAGAGCTAGAT	GTCTTTTAAGGGTGC	NCNCAGACACAGC	230

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 06:21:19 ; Search time 3407 Seconds
(without alignments)
9369.300 Million cell updates/sec

Title: US-09-913-569b-5
Perfect score: 876
Sequence: 1 gcacgagttctgttcacgcc.....ttttgtgacctctgaaaaa 876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	869	99.2	1082	3	AY106647 Zea mays
2	569.8	65.0	589	4	BG842875 MEST41-A1
3	518.4	59.2	534	2	AW519994 660058D08
4	432.8	49.4	860	9	CG280271 OG0GP83TH
5	432.8	49.4	866	9	CG372852 OG1DS04TH
6	432.8	49.4	977	9	CG171937 PUFKS52TB
7	431.4	49.2	721	8	B2538974 OGAEK73TC
8	367.8	42.0	371	6	CD950747 SAS 153 G
9	335.8	38.3	746	2	BF482583 WHE2301-2
10	304.4	34.7	816	9	CG237557 OGYBD43TH
11	291.6	33.3	751	6	CB674853 OSJNE10C
12	289.4	33.0	622	6	CA755886 BRO300300
13	285	32.5	705	6	CA755891 BRO60013A
14	284.2	32.4	540	6	CF335095 JMT-04-K
15	279.4	31.9	676	7	D23846 RICO374A R
16	277	31.6	698	5	BQ294856 WHE2855 B
17	277	31.6	704	7	CN012865 WHE3953_H
18	276.2	31.5	595	5	BQ246171 TAB15015C
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21	275.4	31.4	694	6	CD937116 OV.106A24
22	275	31.4	453	1	AU223390 AU223390
23	273.8	31.3	618	6	CA497973 WHE3236_F
24	273.6	31.2	508	4	BJ222340 BJ222340

25	271.8	31.0	607	5	BU984956	BU984956 HF05K17r
26	271.8	31.0	626	5	BQ459983	BQ459983 HA07111r
27	271.8	31.0	654	1	AJ432364	AJ432364 AJ432364
28	271.8	31.0	1114	7	CK166470	CK166470 FGAS05061
29	271	30.9	526	1	AL808244	AL808244 AL808244
30	270.2	30.8	608	4	BJ464274	BJ464274 BJ464274
31	270	30.8	582	6	CA018551	CA018551 HV08P06r
32	269.8	30.8	539	5	BQ765305	BQ765305 EBR003_SQ
33	269.6	30.8	547	6	CD055817	CD055817 HO10F09S
34	269.6	30.8	549	6	CA018844	CA018844 HV09N05r
35	269.6	30.8	671	4	BM371209	BM371209 EBR004_SQ
36	269	30.7	678	4	BJ466724	BJ466724 BJ466724
37	269	30.7	698	2	BF263276	BF263276 HV_C8A000
38	269	30.7	890	2	BE216340	BE216340 HV_C8B001
39	267	30.5	645	2	BE445264	BE445264 WHE1133_A
40	267	30.5	674	4	BJ264621	BJ264621
41	267	30.5	687	6	CD899012	CD899012 G174.110M
42	267	30.5	706	4	BJ308874	BJ308874 BJ308874
43	266.6	30.4	495	2	BE443195	BE443195 WHE1109_C
44	266.2	30.4	560	2	BE446350	BE446350 WHE1455_D
45	266.2	30.4	643	7	CN011503	CN011503 WHE3885_A

ALIGNMENTS

RESULT 1
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LOCUS Zea mays PC0065540 mRNA sequence. 1082 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0065540 mRNA sequence.
ACCESSION AY106647
VERSION AY106647.1 GI:21209725
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Hailey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitgitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1082)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Location/Qualifiers
1..1082
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 99.2%; Score 869; DB 3; Length 1082;